SEQ ID Model		Description	E-value	Score	Repeats	Position
						344:345-
						374:375- 407
1701	URO-D	Uroporphyrinogen decarboxylase (URO-D)	7.8	-229.7	1	79-354
1702	pkinase	Protein kinase domain	0.00012	-68.0	1	31-278
1702	HEAT	HEAT repeat	1.2	15.6	2	342-
						380:499- 537
1705	cyclin	Cyclin, N-terminal domain	3.8e-11	50.5	1	157-279
1708	WD40	WD domain, G-beta repeat	1.5e-11	51.8	5	278-
			1			313:371-
	Į.				l	407:413-
					ł	447:493-
			}			529:535-
1709	SH2	SH2 domain	0.002		ļ	569
1710	abhydrola	alpha/beta hydrolase fold		10.0	1	287-364
	se	, ,	2.2e-20	81.2	1	124-355
1710	abhydrola	Phospholipase/Carboxylesterase	1.2	-84.9	1	179-359
1711	se 2 zf-C3HC4	Zinc finger, C3HC4 type (R1NG finger)	0.002	23.7	1	280-320
1711	PHD	PHD-finger	1.9	-12.4	1	280-320
1712	WD40	WD domain, G-beta repeat	3.2e-18	74.0	5	67-
1/12	WD40	wD domain, G-beta repeat	3.2e-18	/4.0	3	101:123-
						157:164-
						199:209-
			ł	1	1	246:253-
						290
1714	Acyltransf erase	Acyltransferase	0.0011	14.0	1	83-217
1719	helicase_ C	Helicase conserved C-terminal domain	1.2e-19	78.7	1	397-475
1719	DEAD	DEAD/DEAH box helicase	4.6e-07	10.4	1	2-210
1719	IPT	Isopentenyl transferase	7.9	-160.7	1	17-172
1720	Na Ca E	Sodium/calcium exchanger protein	8e-76	265.3	2	109-
	x	,				249:471-
						616
1720	DUF205	Domain of unknown function DUF	5.3	-112.7	1	85-253
1720	Fumarate _rcd_D	Furnarate reductase subunit D	8.4	-49.5	1	518-620
1721	vwa	von Willebrand factor type A domain	9.6e-29	108.9	1	34-205
1721	fn3	Fibronectin type III domain	3e-15	64.1	2	212-
						287:332-
						413
1724	pkinase	Protein kinase domain	1.6e-06	-41.3	1	40-359
1725	BRCT	BRCA1 C Terminus (BRCT) domain	1e-15	65.6	3	3-93:642-
						730:753-
						833
1727	BRCT	BRCA1 C Terminus (BRCT) domain	7.2	1.2	1	45-130
1728	rrm	RNA recognition motif.	1.1e-05	32.4	2	545-
						612:880-
1700	-COOOT'	7' F 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.010	20.0		942
1728	zf-CCCH PW1	Zinc finger C-x8-C-x5-C-x3-H type PWI domain	0.012	22.2	1	285-311
1728			0.047	-0.6	1	6-78
1730	PX PNAPOR C	PX domain	2.5e-31	117.5	1	94-211
1731		PMP-ZZ/EMP/MP20/Claudin family	1.56-56	201.3	1	1-157
1731	PMP22_C laudin	PMP-22/EMP/MP20/Claudin family	1.5e-56	201.3	1	

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1733	homeobox	Homeobox domain	0.00037	21.6	1	268-339
1733	Vac_Fusi on	Chordopoxvirus fusion protein	5.2	-21.5	1	286-364
1733	CUT	CUT domain	8.5	-38.0	1	159-240
1734	homeobox	Homeobox domain	0.00037	21.6	1	268-339
1734	Vac_Fusi on	Chordopoxvirus fusion protein	5.2	-21.5	1	286-364
1734	CUT	CUT domain	8.5	-38.0	1	159-240
1738	efhand	EF hand	1.5e-16	68.4	2	40-68:76- 104
1742	trypsin	Trypsin	6.5	-55.6	1	33-255
1743	Exonuclea se	Exonuclease	1.2e-36	135.2	1	39-213
1745	Smr	Smr domain	0.0029	13.0	1	1594-1672
1745	RyR	RyR domain	1.5	-29.0	1	1312-1403
1745	L27	L27 domain	3.6	5.1	1	1573-1626
1746	Smr	Smr domain	0.0029	13.0	1	1611-1689
1746	RyR	RyR domain	1.5	-29.0	1	1312-1403
1746	L27	L27 domain	3.6	5.1	1	1590-1643
1746	Smg4_UP F3	Smg-4/UPF3 family	9.7	-74.5	1	1379-1518
1747	mito_carr	Mitochondrial carrier protein	1.3e-81	284.5	3	1-90:98- 198:200- 288
1748	OSCP	ATP synthase delta (OSCP) subunit	8.4	-94.4	1	67-213
1749	Oxysterol BP	Oxysterol-binding protein	3.4e-78	273.2	1	488-875
1749	PH	PH domain	2.2e-09	44.6	1	52-146
1750	lactamase B	Metallo-beta-lactamase superfamily	4.1	-28.9	1	1-153
1751	lipoxygen ase	Lipoxygenase	9.5c- 133	454.4	1	126-703
1751	PLAT	PLAT/LH2 domain	1.6e-33	124.8	1	2-116
1753	Rho_GD1	RHO protein GDP dissociation inhibitor	3.2e- 113	389.5	1	1-187
1756	GRAM	GRAM domain	7.5c-17	69.4	1	110-177
1757	homeobox	Homeobox domain	3.6e-29	110.3	1	21-77
1758	lipocalin	Lipocalin / cytosolic fatty-acid binding pr	1.1c-24	95.4	1	38-168
1759	ig	Immunoglobulin domain	3.1e-13	57.4	2	35- 112:160- 234
1761	oxidored_ q1	NADH-Ubiquinone/plastoquinone (complex I)	0.078	-128.7	1	16-259
1761	DUF250	Domain of unknown function, DUF250	0.45	-85.1	1	162-337
1761	DUF6	Integral membrane protein DUF6	2.5	-14.8	1	192-328
1761	secY	eubacterial secY protein	7.2	-246.6	1	36-243
1761	FecCD	FecCD transport family	9.8	-221.2	1	120-328
1762	Keratin_B 2	Keratin, high sulfur B2 protein	3.3e-07	32.9	2	11- 113:114- 204
1763	sugar_tr	Sugar (and other) transporter	0.018	-119.2	1	43-449
1763	oxidored_ q1	NADH-Ubiquinone/plastoquinone (complex I)	4.7	-165.1	1	146-442
1765	VPS9	Vacuolar sorting protein 9 (VPS9) domain	4.5e-33	123.3	1	380-484
1765	RA	Ras association (RalGDS/AF-6) domain	0.73	-5.9	1	518-607

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1766	SSF	Sodium:solute symporter family	5.9c-	697.6	1	106-535
			206			
1766	oxidored_ q1	NADH-Ubiquinone/plastoquinone (complex 1)	4.8	-165.2	1	216-521
1766	MIP	Major intrinsic protein	5.8	-121.9	1	112-364
1766	DsbD	Cytochrome C biogenesis protein	8.6	-97.3	1	195-425
		transmemb				
1767	Peptidase M3	Peptidase family M3 .	1.3e- 203	689.8	1	251-701
1768	RasGAP	GTPase-activator protein for Ras-like	1.3e-26	101.9	1	449-621
1768	PH	PH domain	0.012	22.2	1	112-236
1768	C2	C2 domain	2.6	-10.9	1	249-332
1768	Tymo_45 kd 70kd	Tymovirus 45/70Kd protein	4.2	-293.9	1	561-979
1768	RNA pol	DNA-dependent RNA polymerase	5.1	-234.7	1	381-1225
1768	PHD	PHD-finger	6.9	-17.6	fi	214-273
1770	rrm	RNA recognition motif.	0.48	5.6	2	238-
						323:352- 422
1772	zf-C2H2	Zinc finger, C2H2 type	1.6e-87	304.2	13	49-71:197 219:225- 247:253- 275:281- 303:309- 331:337- 359:365- 387:393- 415:421- 443:449- 471:477- 499:505- 527
1772	zf-BED	BED zinc finger	8.9	-6.9	1	490-528
1773	ATP-	ATP synthase subunit C	5.4e-08	40.0	i	62-127
	synt_C				}	
1774	zf-B_box	B-box zinc finger	7.2e-14	59.5	1	90-131
1774	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.6e-10	48.4	1	15-58
1774	PHID	PHD-finger	1.1	-10.3	1	14-61
1774	zf-AN1	AN1-like Zinc finger	1.4	-3.2	1	15-53
1774	zf-UBR1	Putative zinc finger in N-recognin	7.6	-23.6	1	93-146
1775	FH2	Formin Homology 2 Domain	5.4e-50	179.5	1	21-455
1775	WH2	WH2 motif	0.0058	23.3	1	441-456
1777	PHID	PHD-finger	8.7	-18.6	1	493-522
1779	Branch	Core-2/I-Branching enzyme	3.9e-05	-52.8	1	175-516
1780	TFIIS	Transcription factor S-II (TFIIS)	3.9	-3.7	1	295-344
1781	SH3	SH3 domain	1.3e-13	58.6	1	454-508
1782	filament	Intermediate filament protein	3.9	-200.0	1	134-406
1783	SET	SET domain	2e-53	190.9	1	3878-4006
1783	PHD	PHD-finger	4.7e-28	106.6	3	20-71:72- 118:147- 200
1783	HMG_bo	HMG (high mobility group) box	0.0047	12.3	1	710-773
1783	DC1	DC1 domain	8.5	1.7	3	19-50:69- 98:146-176
1784	zf-DHHC	DHHC zine finger domain	2.4e-25	97.7	1	90-154
1785	zf-C2H2	Zinc finger, C2H2 type	9.3e-14	59.1	4	18-40:64-
			2.30-1-7	57.1		86:92-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						115:178-
						200
1788	ion_trans	Ion transport protein	8.3e-18	72.6	1	438-672
1788	ank	Ankyrin repeat	1.9e-06	34.8	2	77-
						108:163- 195
1788	Srg	C.elegans Srg family integral	8.1	-222.4	1	418-669
1,00	U.S.	membrane prot	0.1	-222.7	l *	410-009
1791	ubiquitin	Ubiquitin family	0.0036	24.0	1	124-195
1792	Gag p10	Retroviral GAG p10 protein	4e-23	90.2	ì	1-89
1798	Ribosoma 1 S12	Ribosomal protein S12	0.003	-14.2	1	7-66
1799	efhand	EF hand	1.1e-07	39.0	3	281-
						309:318-
						346:353-
						381
1799	Acyltransf erase	Acyltransferase	0.0001	26.8	1	18-203
1801	zf-C2H2	Zinc finger, C2H2 type	3.2e-79	276.6	12	160-
						182:188-
						210:216-
						238:244-
						294:300-
						322:355-
			1			377:431-
			1			453:459-
	l		-		!	481:487-
						509:515-
						537:543-
						565
1801	LIM	LIM domain	4.7	-17.4	1	433-487
1802	lectin_c	Lectin C-type domain	1.4e-25	98.4	1	143-250
1802	lectin_c	Lectin C-type domain	1.4e-25	98.4	1	143-250
1804	efhand	EF hand	2,5e-08	41.1	2	16-44:56- 82
1806	LRR	Leucine Rich Repeat	1.5e-07	38.5	5	130-
						151:152-
						173:174-
	1					195:196-
						217:221- 243
1807	COX3	Cytochrome c oxidase subunit III	3.5	-233.2	1	51-219
1807	CbiM	CbiM	9.2	-93.3	1	114-249
1807	oxidored_	NADH-ubiquinone oxidoreductase	9.8	-59.5	1	89-169
	q5_N	chain 4				
1808	Sulfotrans	Sulfotransferase protein	6.6	-108.5	1	39-282
1814	fer Metalloph	0.1.	0.23	14.3	1	26.244
	os	Calcineurin-like phosphoesterase	1		_	36-241
1815	rrm	RNA recognition motif.	0.67	4.1	1	201-269
1816	filament	Intermediate filament protein	1.5	-188.9	1	1-253
1817	MAGE	MAGE family	4.2e-17	70.3	2	14-
			1			613:655-
						867
1817	Atrophin-	Atrophin-1 family	9.5	-684.8	1	4-783
1818	1 Tropomod	Tropomodulin	8.1	169.0	1	202.002
1818	ropomod	ropomodulin	8.1	-168.0	1	362-653

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	ulin					
1819	Hydrolase	haloacid dehalogenase-like hydrolase	3.4c-21	83.8	1	28-282
1820	Fe_hyd_l g_C	Iron only hydrogenase large subunit, C- te	1.3e-92	321.1	1	204-516
1820	Fe_hyd_S SU	Iron hydrogenase small subunit	8.3	-13.1	1	529-576
1821	filament	Intermediate filament protein	1e-143	490.8	1	55-366
1822	Keratin_B	Keratin, high sulfur B2 protein	0.082	-51.3	1	12-174
1824	metalthio	Metallothionein	5.7e-17	69.8	1	48-108
1824	AFP	Insect antifreeze protein	2.6	14.5	1	61-72
1825	C2	C2 domain	4.7e-53	189.7	2	373- 462:528- 617
1825	RPH3A_e ffector	Rabphilin-3A effector domain	0.035	-127.1	1	1-237
1825	zf-MlZ	MIZ zinc finger	0.4	-10.5	1	80-111
1825	PHD	PHD-finger	0.97	-9.7	1	62-108
1825	LIM	LIM domain	2.2	-14.6	1	80-128
1825	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.1	-4.0	1	63-105
1828	efhand	EF hand	8.4e-08	39.4	3	106- 134:142- 170:407- 435
1829	60s_ribos omal	60s Acidic ribosomal protein	7.4	-38.2	1	163-291
1831	Tektin	Tektin family	1.6	-227.3	1	1-150
1833	EGF	EGF-like domain	1.1e-32	122.0	5	26-54:57- 85:92- 124:156- 187:194- 226
1833	laminin_E GF	Laminin EGF-like (Domains III and V)	1.6	-5.9	1	29-63
1833	Bowman- Birk_leg	Bowman-Birk serine protease inhibitor	4.8	-16.7	1	37-85
1833	metalthio	Metallothionein	5.5	-10.1	1	59-117
1834	7tm_1	7 transmembrane receptor (rhodopsin family)	4.8e-05	-0.8	1	31-273
1834	7tm_2	7 transmembrane receptor (Secretin family)	5.5	-151.6	1	9-248
1835	rrm	RNA recognition motif.	0.05	15.7	1	75-141
1835	Mct_10	Met-10+ like-protein	0.065	-100.4	1	333-583
1835	UPF0020	Putative RNA methylase family UPF0020	0.073	-53.8	1	410-566
1835	PCMT	Protein-L-isoaspartate(D-aspartate) O-	0.2	-114.1	1	391-543
1835	Methyltra nsf 4	Putative methyltransferase	2.1	-82.0	1	424-566
1835	notch	Notch (DSL) domain	6.1	-10.5	1	233-271
1836	Kelch	Kelch motif	3e-33	123.9	4	242- 288:290- 331:333- 378:380- 435
1836	BTB	BTB/POZ domain	2.3	-15.2	1	1-129
1837	tsp_l	Thrombospondin type 1 domain	0.0014	23.3	5	139- 196:203- 256:257-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						313:320-
						370:374-
						432
1837 1838	EB	EB module	6.4	-10.5	1	330-399
1838	adh_zinc Lipase G	Zinc-binding dehydrogenase Lipase/Acylhydrolase with GDSL-like	7.3e-55 5.5	195.7 -20.4	1	44-369 103-189
	DSL	motif			1	
1839	pkinase	Protein kinase domain	2.4e-05	-58.0	1	81-333
1841	zf-C2H2	Zinc finger, C2H2 type	4.4e-30	113.4	7	141-
						163:169-
	1					191:197- 219:225-
						247:350-
						372:378-
	l		1			400:406-
						434
1841	KRAB	KRAB box	5.1e-23	89.9	1	44-84
1841	TF11S	Transcription factor S-II (TFIIS)	2.4	-1.9	1	144-179
1841	Lentiviral Tat	Lentiviral Tat protein	4.9	-23.0	1	35-125
1841	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.2	-7.1	1	352-411
1841	rubredoxi n	Rubredoxin	7.4	-11.1	1	403-433
1842	E2F_TDP	Transcription factor E2F/dimerisation partne	1.5	-95.1	1	18-229
1843	V_ATPas e sub a	V-type ATPase 116kDa subunit family	0	1258.7	1	26-831
1843	UCR_14k D	Ubiquinol-cytochrome C reductase compl	3.2	-40.4	1	6-112
1843	FliP	FliP family	4.8	-148.9	1	533-661
1843	PsbH	Photosystem II 10 kDa phosphoprotein	7.1	5.1	1	751-803
1844	aa_perme ases	Amino acid permease	5.60-08	-125.3	1	28-529
1844	Aa_trans	Transmembrane amino acid transporter pro	0.71	-178.9	1	30-408
1844	BPD_tran sp 2	Branched-chain amino acid transport syst	3.3	-116.9	1	175-440
1844	MVIN	Virulence factor MVIN	3.5	-240.9	1	87-515
1844	FecCD	FeeCD transport family	5.3	-216.0	1	311-521
1844	ion_trans	Ion transport protein	6.2	-11.7	1	288-495
1844	7tm_5	7TM chemoreceptor	7.1	-168.6	1	238-498
1848	sugar_tr	Sugar (and other) transporter	0.0072	-107.9	1	12-407
1848	xan_ur_pe rmease	Permease family	5.6	-196.7	1	38-359
1848	FecCD	FecCD transport family	6.3	-217.4	1	56-287
1848	Nucleosid e tran	Nucleoside transporter	8.1	-162.4	1	82-365
1848	PUCC	PUCC protein	9.8	-283.2	1	51-403
1849	Filamin	Filamin/ABP280 repeat	2.3e-20	81.1	1	396-494
1849	zf-B_box	B-box zinc finger	9.3e-11	49.2	2	130-
						176:186- 227
1849	zf-C3HC4	Zinc finger, C3HC4 type (R1NG finger)	0.0016	24.4	1	29-62
1853	ank	Ankyrin repeat	1.1e-98	341.3	10	485-
						517:518-
						550:551-
						583:584-
						616:617-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						650:651-
			i			683:684-
	I					716:717-
						749:750-
						780:782-
						814
1853	pkinase	Protein kinase domain	1.6e-50	181.3	1	22-286
1854	ras Acvltransf	Ras family	1.4e-13	17.8	1	5-194
	erase	Acyltransferase	3e-34	127.2		92-289
1856	wap	WAP-type (Whey Acidic Protein) 'four-disulfi	0.0025	18.7	1	31-72
1857	arf	ADP-ribosylation factor family	2.5e-11	24.6	1	7-193
1857	GTP_EFT	Elongation factor Tu GTP binding domain	1.6	-82.5	1	19-198
1858	zf-C2H2	Zinc finger, C2H2 type	2.1c-09	44.7	5	82-
10.50	21-02112	Zine ringer, GZF12 type	2.10-05		-	104:110-
					ĺ	132:138-
i						161:364-
	l					386:392-
						416
1858	PHD	PHD-finger	7.7	-18.1	1	365-400
1859	zf-C2H2	Zinc finger, C2H2 type	7.2e-20	79.4	4	119-
	ŀ					141:147-
	!					169:175-
						198:214-
1860	BTB	BTB/POZ domain	1.00	****		237
1860	zf-C2H2	Zinc finger, C2H2 type	1.7e-29 5.1e-14	111.4	3	22-126 373-
1800	ZI-CZF12	Zinc Iniger, CZF12 type	3.16-14	00.0	3	395:401-
						423:429-
						452
1860	K_tetra	K+ channel tetramerisation domain	0.44	-30.2	1	34-124
1860	zf-BED	BED zinc finger	8.9	-6.9	1	363-396
1861	SNF2_N	SNF2 and others N-terminal domain	2.1e-72	254.0	1	137-473
1861	helicase_ C	Helicase conserved C-terminal domain	1.4c-24	95.1	1	559-632
1861	DEAD	DEAD/DEAH box helicase	0.26	-59.6	1	124-337
1861	SEC-C	SEC-C motif	0.43	13.8	1	426-446
1862	ras	Ras family	2.4e-69	243.8	1	19-217
1862	arf	ADP-ribosylation factor family	4.1e-05	-53.5	1	1-182
1864	rrm	RNA recognition motif.	0.053	15.4	1	129-191
1867	T-box	T-box	4.3e-09	29.9	1	1-92
1870	F-box	F-box domain	1.8	15.0	1	124-171
1871	PH	PH domain	1.1e-13	58.9	1	170-273
1872	isodh	Isocitrate/isopropylmalate	1.4e-	423.9	1	10-383
1873	. 1.	dehydrogenase	123			
	ank	Ankyrin repeat	1.8e-08	41.5	2	39-71:72- 104
1874	ank	Ankyrin repeat	1.8c-08	41.5	2	67-99:100- 132
1875	PAP2	PAP2 superfamily	0.0034	13.0	1	1-107
1876	DUF51	Protein of unknown function DUF51	5.7e-13	52.5	i	107-261
1877	zf-C2H2	Zinc finger, C2H2 type	1.5e-72	254.5	9	285-
			"			307:313-
						335:341-
						363:369-
			1			391:397-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						419:425-
	İ		1			447:451-
	i		1			473:479-
						501:507-
						529
1877	KRAB	KRAB box	2.7e-21	84.2	1	49-89
1877	zf-BED	BED zinc finger	0.74	2.7	1	344-392
1877	TFIIS	Transcription factor S-II (TFIIS)	1.5	-0.0	1	369-407
1877	GATA	GATA zinc finger	2.1	-7.1	1	477-524
1877	LIM	LIM domain	2.5	-15.1	1	371-435
1877	E6	Early Protein (E6)	5.7	-66.7	1	315-402
1878	AAA	ATPase family associated with various	1.3e-62	221.4	1	217-409
1878	Sigma54_ activat	Sigma-54 interaction domain	4.6	-165.4	I	184-365
1879	SSF	Sodium:solute symporter family	4.8e- 170	578.3	1	58-460
1880	SSF	Sodium:solute symporter family	1.3e- 198	673.2	1	58-487
1881	perilipin	Perilipin family	6.7e-53	189.2	1	12-369
1882	aminotran _1_2	Aminotransferase class I and II	7.5e-07	25.0	1	165-515
1883	DSPc	Dual specificity phosphatase, catalytic doma	2.5e-30	114.2	1	54-199
1884	ig	Immunoglobulin domain	7.2e-14	59.5	2	34-
		-	1			111:155-
					!	229
1885	MCM	MCM2/3/5 family	4.6e-12	-67.3	1	106-391
1886	Kelch	Kelch motif	1.8e-63	224.3	6	262-
						306:309-
						356:358-
			1			403:405-
						453:455-
					ł	495:497-
					ĺ	544
1886	BTB	BTB/POZ domain	5.3e-32	119.7	1	26-134
1887	UBA	UBA/TS-N domain	1.9e-05	31.5	1	726-765
1887	rrm	RNA recognition motif.	0.00026	27.8	1	1342-1407
1887	MARCKS	MARCKS family	4.3	-90.8	1	270-571
1888	UBA	UBA/TS-N domain	1.9e-05	31.5	1	726-765
1888	rrm	RNA recognition motif.	0.00026	27.8	1	1303-1368
1888	MARCKS	MARCKS family	4.3	-90.8	1	270-571
1889	UBA	UBA/TS-N domain	1.9e-05	31.5	1	726-765
1889	rrm	RNA recognition motif.	0.00026	27.8	1	1245-1310
1889	MARCKS	MARCKS family	4.3	-90.8	1	270-571
1889	Atrophin-	Atrophin-1 family	6.9	-676.1	1	237-986
1890	Na_H_Ex changer	Sodium/hydrogen exchanger family	2.4e-18	74.4	1	119-520
1890	Na_Ca_E x	Sodium/calcium exchanger protein	3.1	-43.6	1	270-384
1890	7tm_5	7TM chemoreceptor	3.8	-163.7	1	259-503
1890	Abi	CAAX amino terminal protease family	5.9	-25.8	1	309-401
1890	oxidored_ q1	NADH-Ubiquinone/plastoquinone	7.9	-169.7	1	251-502
1891	Acyl-	Cytosolic long-chain acyl-CoA thioeste	8.9e-72	251.9	2	26-
	CoA_hydr					168:200-
	0					336
1891	tRNA ant	OB-fold nucleic acid binding domain	3.5	5.8	1	230-307

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	i					
1892	zf-DHHC	DHHC zinc finger domain	8.6e-18	72.5	1	145-207
1894	SPRY	SPRY domain	4.5e-11	50.2	1	353-474
1894	fn3	Fibronectin type III domain	0.054	17.6	1	165-258
1895	dsrm	Double-stranded RNA binding motif	1.5e-12	55.1	2	229- 293:337- 401
1895	WW	WW domain	0.00016	28.5	1	20-49
1896	SPRY	SPRY domain	9.9e-26	98.9	1	186-301

WO 02/070539

PDB annotation	SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN	SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN		CALCIUM BINDING EHZ, REDBERMAL GROWTH FACTOR REGBPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND EH 2 DOMAIN	CALCIUM BINDING EHD, EPIDERMAL GROWTH FACTOR REGEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN			CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
Coumpound	EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	EPS15; CHAIN: NULL;	BPS15; CHAIN: NULL;	CALCIUM-BINDING PROTEIN RAT ONCOMODULIN IRRO 3	CALCIUM BINDING PROTEIN CALMODULIN (/TR=2=C\$ FRAGMENT COMPRISING RESIDUES 78 - 148 ITRC 3 OF THE INTACT MOLECULE) ITRC 4	CALMODULN; CHAIN: A; RS20; CHAIN: B;
SEQFOL D score								
PMF	1.00	0.88	0.22	0.1	66.0	86.0	0.23	0.15
Verify score	0.77	-0.14	-0.02	0.58	0.72	0.33	-0.21	-0.39
Psi Blast	5.7e-21	I.7e-07	3.8e-05	1.16-31	6.8e-11	1.3e-05	1.5e-05	3.8e-05
END	369	86	345	369	97	348	345	345
STAR T AA	279	4	293	278	6	280	284	293
CHAI	<	∢					<	<
PDB ID	1c07	1c07	1cII	1eh2	1eh2	lrro	ltre	Ivrk
SEQ ID NO:	951	951	951	951	951	951	. 951	951

PDB annotation	METAL BINDING PROTEIN CALCIUM BINDING PROTEIN		CALCIUM BINDING PROTEIN CALCIUM BINDING PROTEIN, MUSCLE PROTEIN	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION	MUSCLE PROTEIN MDE; MUSCLE PROTEIN	CALCIUM BINDING CALCIUM BINDING	SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN	SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN		STRUCTURAL PROTEIN HELIX- TURN-HELIX	CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR
Coumpound	PARVALBUMIN; CHAIN: A;	BINDING PROTEIN SARCOPLASMIC CALCIUM- BINDING PROTEIN 2SCP 3	PARVALBUMIN; CHAIN: A, B	TROPONIN C; CHAIN: NULL;	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	MYOSIN; CHAIN: A, B, C, D, E, F, G, H;	CALCIUM-BINDING PROTEIN; CHAIN: NULL;	EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	CARDIAC TROPONIN C; CHAIN: A;	EPS15; CHAIN: NULL;
SEQFOL D score												
PMF	0.25	0.47	0.05	0.17	0.13	0.18	9.05	1.00	0.90	0.22	0.18	1.00
Verify	-0.13	-0.13	-0.81	0.02	-0.03	-0.05	-0.24	0.77	0.10	-0.02	-0.16	0.58
Psi Blast	3.8e-05	5.7e-06	0.00095	5.7e-05	0.00038	0.0019	0.0038	5.7e-21	5.1e-12	3.8e-05	0.0038	1.16-31
END	348	345	389	377	377	377	389	369	66	345	389	369
STAR T AA	293	283	310	280	280	282	310	279	4	293	280	278
CHAI N ID	∢	A	¥		В	В		¥	Ą		A	
PDB	2pvb	2scp	1a75	1aj4	laui	Ibr.	1bu3	1c07	1007	loll	1dtl	1eh2
SEQ NO ID	156	951	952	952	952	952	952	952	952	952	952	952

PDB annotation	RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN	CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN	GROWTH FACTOR EHI; EH DOMAIN, EPSIS, EF-HAND, SOLUTION STRUCTURE, S100 PROTEIN			CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	METAL BINDING PROTEIN CALCIUM BINDING PROTEIN	
Coumpound		EPS15; CHAIN: NULL;	EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CHAIN: A;	CALCIUM-BINDING PROTEIN RAT ONCOMODULIN IRRO 3	CALCIUM BINDING PROTEIN CALMODULIN (/TR-2-C\$ PRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) ITRC	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN; CHAIN; A; RS20; CHAIN: B;	PARVALBUMIN; CHAIN: A;	BINDING PROTEIN SARCOPLASMIC CALCIUM- BINDING PROTEIN 2SCP 3
SEQFOL D score			- 3						
PMF		0.99	0.80	86.0	0.23	0.49	0.15	0.25	0.47
Verify		0.81	0.64	0.33	-0.21	-0.23	-0.39	-0.13	-0.13
Psi Blast		1.7e-13	1.7e-08	1.3e-05	1.5e-05	0.00038	3.8e-05	3.8e-05	5.7e-06
END		76	97	348	345	377	345	348	345
STAR T AA		e	14	280	284	280	293	293	283
CHAI N ID			¥		٧	V	V	¥	۷ .
PDB TD		1eh2	Iqit	Irro	ltrc	lvrk	Ívrk	2pvb	2scp
SEQ No.		952	952	952	952	952	952	952	952

PDB annotation	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)	COMPLEX (TRANSFERASE/PEPTIDE) ITAM PEPTIDE, COMPLEX (TRANSFERASE/PEPTIDE), SYK, KINASE, SH2 DOMAIN, ITAM		COMPLEX (PROTO- ONCOGNELEALLY PROTEIN) SRC HOMOLOGY 2 DOMAIN; SH2 DOMAIN, SIGNAL TRANSDUCTION, PEPTIDE COMPLEX, 2 COMPLEX (PROTO-ONCOGENEEARLY PROTEIN)		SH2 DOMAIN PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY ALPHA SH2
Coumpound	C-SRC TYROSINE KINASE; CHAIN: A, B, ACE-FORMYL PHOSPHOTYR-GLU-(N,N- DIPENTYL AMINE); CHAIN: C, D:	SYK KINASE; CHAIN: A, C, E, G, I, K; T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN; CHAIN: B, D, F, H, J, L;	TRANSFERASE(PHOSPHOTRA NSFERASI) PROTO- ONCOGENE TYROSINE KINASE (E.C.7.1.112) 1482 3 (SRC HOMOLOGY 2 DOMAIN) (ABELSON, SITS ARGI) 1482 5 (NMR, 20 STRUCTURES) 14B2 5	FYN PROTEIN-TYROSINE KINASE, CHAIN: E; PHOSPHOTYROSYL PEPTIDE; CHAIN: P	HYDROLASE(SHZ DOMAIN) TYROSNIE PHOSHATIASE SYP (N-TERMINAL SHZ DOMAIN) LAYA 3 (PTPL), SHPTP2) (E.C.J. 3.48) COMPLEXED WITH THE PETIDE LAYA 4 PDGRE-1091 LAYA 5	P85 ALPHA; CHAIN: NULL;
SEQFOL D seare						
PMF	86.0	0.72	0.63	0.99	0.1	0.82
Verify score	0.34	0.27	0.02	0.46	0.18	0.36
Psi Blast	3.8e-17	1.5e-18	3.8e-17	1.7e-17	7.6e-18	3.8e-19
END	413	413	417	413	412	418
STAR T AA	319	255	319	319	317	319
CHAI N ID	¥	∢	_	íz,	A	
EDB CI	1a09	1881	1ab2	laot	laya	1bfi
SEQ No. 15	953	953	953	953	953	953

			_		-	
DOMAIN, P85ALPHA, PI 3-KINASE, NMR, C TERMINAL SH2 2 DOMAIN	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE) PROTEIN-TYROSINE KINASE SHZ DOMAIN, COMPLEX 2 (PHOSPHOTRANSFERASE/PEPTITIE)	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COLLED-COILS, STRUCTURAL PROTEIN	GENE REGULATION SH2 DOMAINS	SIGNALING PROTEIN SLAM; SH2 DOMAIN, TYROSINE KINASE, SIGNAL TRANSDUCTION, PEPTIDE 2 RECOGNITION	SH2 DOMAIN GRB2; GRB2, SH2 DOMAIN, PROTEIN NMR, SOLUTION STRUCTURES	
	SYK PROTEIN TYROSINE KINASB; CHAIN: A; ACETYL- THR-PTR-GI.U-THR-LEU-NH2; CHAIN: B;	ALPHA SPECTRIN; CHAIN: A, B, C;	SAP SH2 DOMAIN; CHAIN: A, B, C, D;	T CELL SIGNAL TRANSDUCTION MOLECULE SAP, CHAIN: A; SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE: CHAIN: B:	GROWTH FACTOR RECEPTOR BOUND PROTEIN-2; CHAIN: NULL;	HEOSPHOGUESTER HYDROLASE PHOSPOLIANS CAGNAMA-1 (E.C.11.4.11) (CCANAMA-1 (
					58.62	
	0.82	90.00	0.49	0.75		0.49
	0.33	0.05	0.04	0.22		0.32
	3.8e-19	0.00013	5.7e-18	1.96-19	0.0017	9.5e-19
	416	228	413	413	425	417
	319	140	320	319	312	319
	∢	<	я	<		∢
	losy	1cun	zlbi	1d4t	1ths	2pld
	953	953	856	953	953	953
	DOMÁIN, PSSALPHA, PI 3-KINASE, NMR, C TERMINAL SH2 2 DOMAIN	Losy A 319 416 3.8e-19 0.33 0.82 SYK PROTEIN TYROSINE KINASE CHAIN AGETYL THE PERGLU-THR-LEU-NH2, CHAIN: B; CHAIN: B;	Losy A 319 416 3.8e-19 0.33 0.82 SYK PROTEIN TYROSINE KINASE, CHAIN A, ACETYL THR. PTRG.L.T.THRLEUNH2, CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: CHAIN: A; CH	Losy A 319 416 3.8e-19 0.33 0.82 SYK PROTEIN TYROSINE Item A 140 228 0.00013 0.05 0.06 ALPH SPECTRIN; CHAIN; A, B, C, A 140 228 0.00013 0.05 0.06 ALPH SPECTRIN; CHAIN; A, B, C,	Losy A 319 416 3.8e-19 0.33 0.82 SYK_PROTEIN TYROSINE I.Om A 140 228 0.00013 0.05 0.06 ALPHA SPECTRIN; CHAIN: A, B, C, D, C,	Losy A 319 416 3.8±19 0.33 0.82 SYK PROTEIN TYROSINE I.Com A 140 228 0.00013 0.05 0.06 ALPH SPECTRIN; CHAIN: B, C,

PDB annotation		COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)	COMPLEX (TRANSFERASE/PEPTIDE) ITAM PEPTIDE; COMPLEX (TRANSFERASE/PEPTIDE), SYK, KTMASE, SH2 DOMAN ITAM		COMPLEX (PROTO- ONCOGENERARY PROTEIN) SRC HOMOLOGY 2 DOMAIN; SHZ DOMAIN, SIGNAL TRANSDUCTION, PET IDE COMPLEX, 2 COMPLEX (PROTO-ONCOGENEZARLY PROTEIN)	
Coumpound	PRO-LEU-PRO-ASP-PRO-LYS) (NMR, MINIMIZED AVERAGE STRUCTURE) 2PLD 7	C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,IN- DIPENTYL AMINE); CHAIN: C, D.	SYK KINASE; CHAIN: A, C, E, G, I, K; T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN; CHAIN: B, D, F, H, J, L;	TRANSFERASE(PHOSPHOTRA NSFERASE) PROTO- ONCOGENE TYROSINE KINASE (E.C.Z.II.12) 1AB2 3 (SRC HOMOLOGY 2 DOMAIN) (ABELSON, SITS AB1) 1AB2 4 (NMR, 20 STRUCTURES) 1AB2 4	FYN PROTEIN-LYROSINE KINASIE, CHAIN: I; PHOSPHOTYROSYL, PEPTIDE; CHAIN: P	HYDROLASE(SI12 DOMAIN) TYROSINE PHOSPHATASE SYP (N-TERMINAL SH2 DOMAIN) IAYA 3 (PTPID, SHPTP2) (E.C.3.1.348) COMPLEXED WITH THE PEPTIDE IAYA 4
SEQFOL D score						
PMF score		86:0	0.72	0.63	0.99	0.1
Verify score		0.34	0.27	0.02	0.46	0.18
Psi Blast		3.8e-17	1.5e-18	3.8e-I7	1.7e-17	7.6e-18
END		440	440	<u>*</u>	440	439
STAR T AA		346	282	346		344
CHAI N ID		4	4		ř.	<
FDB ID		1a09	la81	lab2	laot	laya
SEQ NO:		954	954	954	954	954

PDB annotation		SH2 DOMAIN PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY ALPHA SH2 DOMAIN, PRSALPHA, PI 3-KINASE,	COMPLEX (PHOSPHOTRANSFERASEPEPTIDE) PROTEIN-TYROSINE KINASE SH2 PROTEIN-TYROSINE ANSPERTA	1	SIGNALING PROTEIN SLAM, SH2 DOMAIN, TYROSINE KINASE, SIGNAL TRANSDUCTION, PEPTIDE 2 RECOGNITION		
Coumpound	PDGFR-1009 LAYA 5	P85 ALPHA; CHAIN: NULL;	SYK PROTEIN TYROSINE KINASE; CHAIN: A; ACETYL- THR-PTR-GLU-THR-LEU-NH2; CHAIN: B;	SAP SH2 DOMAIN; CHAIN: A, B, C, D;	T CELL SIGNAL TRANSDUCTION MOLECULE SAP, CHAIN: A; SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE: CHAIN: B;	PHOSPHOLD IDESTIRS HYDROLASE PROSPOLIANS CGAMMAL 16.C.1.1.4.11) (C. CGAMMAL STE 201.0.3 DAMAIN CONFRENCE RESIDIES 66.753 CONFLEXED WITH A 201.0.4 RESIDIES 66.753 CONFLEXED WITH A 201.0.4 RESIDIES 66.753 RES	
SEQFOL D score							
PMF		0.82	0.82	0.49	0.75	0.49	
Verify		0.36	0.33	0.04	0.22	0.32	
Psi Blast		3.8e-19	3.8e-19	5.7e-18	1.9e-19	9.5e-19	
END		445	443	440	440	444	
STAR T AA		346	346	347	346	346	
CHAI N ID			V.	В	∢	¥.	
PDB ID		16fi	lcsy	Idlz	1d4t	2pid	_
SEQ NO:		954	954	954	954	954	_

PDB TD	CHAI N ID	STAR T AA		Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
<	_	35	427	1.7e-77			150.38	REGULATOR OF CHROMOSOME CONDENSATION I; CHAIN: A, B, C;	GUIANDE UUCLGOTIDE EXCHANGE PACTOR RCC1; GUANDE E NUCLEOTIDE EXCEANGE BACTOR, GEF, RAN; 2 RAS-LIKE NUCLEAR GITP BINDING PROTEIN HEADER TER
`	∢	51	423	1.7e-77	0.69	1.00		REGULATOR OF CHROMOSOME CONDENSATION I; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE PACTOR RCCI; GUANTINE NUCLEOTIDE EXCHANGE PACTOR, GEF, RAN, 2RAS-LIKE NUCLEAR, GTF BINDING PROTEIN HEADER TER
_									
۹.	∢	8	183	9.0000	-0.16	0.05		PROLINE IMINOPEPTIDASE; CHAIN: A, B;	AMINOPEPTIDASE AMINOPEPTIDASE, PROLINE IMINOPEPTIDASE, SRINE PROTEASE, 2 XANTHOMONAS CAMPESTRIS
		991	204	0.00038	-0.67	0.49		TRIACYI.GLYCEROL HYDROLASE; CHAIN: NULL;	HYDROLASE TRIACYLGLYCEROL- HYDROLASE, X-RAX CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANDO, CIS-PEPTIDE,
_	A	98	204	7.6e-05	0.14	0.57		PALMITOYL PROTEIN THIOESTERASE 1; CHAIN: A;	HYDROLASE ALPHA/BETA HYDROLASE, GLYCOPROTEIN
	Q	165	204	0.0048	-0.60	0.23		TRIACYL-GLYCEROL- HYDROLASE; CHAIN: D, E;	LIPASE LIPASE, LIPASE, HYDROIASE, PSEUDOMONDACEAE, COVALENT INTERMEDIATE, 2 TRIGI YCERIDE ANALOGUE, ENANTIOSELECTIVITY
+									
_	<	2	121	3.80-38	0.57	00.1		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION,

PDB CH	CHAI N ID	STAR T AA	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
_	l							-	UBIQUITIN-CONJUGATING ENZYME
layz A		2	121	3.8e-38			124.83	UBIQUITIN-CONJUGATING ENZYME RADG; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
layz A	l	2	121	5.1e-37	0.63	00'1		UBIQUITIN-CONIUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
lqcq A		1	611	3.4e-40	0.62	00'1		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN- CONJUGATING ENZYME, YEAST
Iqcq A		3	120	3,46-40			70.02	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN- CONJUGATING ENZYME, YEAST
2aak		-	611	3.4e-37	0.59	00'1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBCI; UBIQUITIN CONJUGATION, LIGASE
2aak		-	120	3.4e-37			141.95	UBIQUITIN CONJUGATING ENZYMB; CHAIN: NULL;	UBIQUITIN CONTUGATION UBC1; UBIQUITIN CONTUGATION, LIGASE
layz A		2	136	1.5e-46	1.15	1.00		UBIQUITIN-CONIUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
layz A		2	136	1.9e-48	0.91	00'1		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
layz A		2	136	1.9e-48			162.79	UBIQUITIN-CONJUGATING ENZYME RAD6, CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBCZ; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
lded A		1	134	05-95.1	69'0	00'1		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN- CONUGATING ENZYME, YEAST
Iqcq A		3	135	1.5e-50			102.58	UBIQUITIN CONJUGATING	LIGASE UBIQUITIN, UBIQUITIN-

PDB annotation	CONJUGATING ENZYME, YEAST	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE	UBIQUITIN CONTUGATION UBC1; UBIQUITIN CONTUGATION, LIGASE	MOTION OF STREET, A SOURCE OF COTTON	ATPASE, MICROTUBULE ASSOCIATED	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED	CONTRACTILE PROTEIN NCD,	CLARET SEGREGATIONAL PROTEIN: NCD CRYSTAL	STRUCTURE, MICROTUBULE	MOTORS, KINESIN 2 SUPERFAMILY,	CONTRACTOR DESCRIPTION	CLARET SEGREGATIONAL	PROTEIN; NCD CRYSTAL	STRUCTURE, MICROTUBULE	MOTORS, KINESIN 2 SUPERFAMILY,	CONTRACTILE INCIDENT	CLARET SEGREGATIONAL	PROTEIN; NCD CRYSTAL	STRUCTURE, MICROTUBULE	MOTORS, KINESIN 2 SUPERFAMILY,	CONTRACTILE PROTEIN	ENDOCYTOSIS/EXOCYTOSIS	COMPLEX, MULTI-SUBUNIT	TRANSCRIPTION INHIBITIOR BETA-
Coumpound	ENZYME; CHAIN: A;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	vamon: Grand and	MINDSIN, CHAIN: NOLL;	KINESIN; CHAIN: NULL;	MICROTUBULE MOTOR	PROTEIN NCD; CHAIN: A, B, C, D:	î		MCDOWINITE MOTOR	PROTEIN NCD; CHAIN: A, B, C,	Ď;			MICROTTIBILE MOTOR	PROTEIN NCD; CHAIN: A, B, C.	ď			A STATE OF THE STA	SYNIAXIN BINDING PROTEIN	I; CHAIN: A; SYNIAXIN IA; CHAIN: B;	TRANSCRIPTIONAL
SEQFOL D score			179.88	20200	55.102						120.50	00.651												
PMF		1.00				1.00	1.00									001					0.0	e.18		96.0
Verify score		88.0				0.39	0.33									0.34					.,	CT.0		0.54
Psi Blast		3.4e-48	3.4e-48		,	0	1.7e-81				1 70 00	1.10-70				1.7e-98						1.3e-15		1.7e-78
END		134	135		5	371	372				277	3				372	!				000	628		1643
STAR T AA		1	-	,		7	5				7					6					677	ŧ		1269
CHAI				Ī			4									Ą						n		¥
ED CI		2aak	2aak	5	di .	Ibg2	1cz7				Lory	7				Icz7					1.77	<u></u>		leri
SEQ NO:		963	963	120		126	126				071	:				971					120	1/6		97.1

1 PDB annotation	HAIN: A, PROPELLER	A COMPLEX (CONTEX CONTEX CONTE	A COMPLEX CORP GAPACA; BINDING TRANSDICCIR BETAL, GAMAA; TRANSDICCIR BETAL SHENIT; GAMAA; TRANSDICOR GAMAA BINDING TRANSDICOR GAMAA BINDING TRANSDICOR SI SIGNAT, SIGNAT, SI SIGNAT, SI SIGNAT, SI SIGNAT, SI SIGNAT, SI SI SI SI SI SI SI SI SI SI					-
Coumpound	REPRESSOR TUPI; CHAIN: A, B, C;	GTALPHAGOLAIPHA CHIMERA, CHAIN: A; GT- BETA, CHAIN: B; GT-GAMMA; CHAIN: G;	GTALIPHA GI-AIPHA CHMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	GT-ALPHA/GI-ALPHA GUDERA, CHAIN: B; GT-GAMMA; CHAIN: G;	KINESIN; CHAIN: A, B;	KINESIN; CHAIN: A, B;	KINESIN; CHAIN: A, B;	KINESIN MOTOR NCD; CHAIN:
SEQFOL D score		115.67			135.00			
PMF			00'1	0.1		1.00	0.99	1.00
Verify			0.88	0.42		60.0	-0.48	0.34
Psi Blast		1e-98	1c-98	3.4e-46	1.5e-71	1.5e-71	1.7e-36	1e-81
END		1600	1640	1660	260	281	380	370
STAR		1229	1317	1429	3	7	296	2
CHAI		m	m.	щ	V	V	В	٧
EDB CL		lgot	1got	1got	2kin	2kin	2kin	2ncd
SEQ NO: D		971	971	971	971	971	971	971

									_	
PDB annotation	NCD, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P. 1,00P, MCROTHINI, ILE RINDING	PROTEIN	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P. LOOP, MICROTUBULE BINDING PROTEIN	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED ROTTEIN, MOTOR 2 PROTEIN, ATPASE, P. LOOP, MICROTUBLIE BINDING PROTEIN	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON		GENE REQUIATION POZ DOMÁNIS; PROTBIN-PROTBIN INTERACTION DOMÁNIN, TRANSCRIPTIONÁL 2 REPRESSOR, ZINC-PINGER PROTBIN, X-RA P. ROTBIN, X-RA P. CRYSTALLOGRAPHY, 3 PROTBIN STRUCTURE, PROMYTILOCYTIC
Coumpound	PRINCES ACCROMINATION OF TARREST	KINESIN MOTOR NCD; CHAIN: A;	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;
SEQFOL D score	2000	132.55	165.99							
PMF					1.00	1.00	1.00	1.00		1.00
Verify score					0:30	0.19	-0.23	-0.39		0.20
Psi Blast	1- 01	Ie-81	1,9e-91		Ie-83	1.90-91	3.8e-35	6.8e-28		1.7e-20
END AA	141	3/1	370		370	370	380	405		125
STAR T AA		,	8		8	٥	298	298		in.
CHAI N ID		٧					В	В		<
PDB	-	pour.	3kar		3kar	3kar	3kin	3kin		onqı
SEQ NO:	120	3/1	11/6		971	1/6	126	97.1		975

PDB annotation	LEUKEMIA, GENE REGULATION	GENE REGILA, TION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, ITA-MSCRIPTIONAL 2 REPRESOR, ZINC-FINGER PROTEIN, X-RAV CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYZLOCYTIC LEUKEMIA, GENE REGULATION	GENE REGULATION POZ DOMANN; PROTEIN-PROTEIN INTERACTION DOMAN, TRANSCRIPTIONAL 2 REPRESOR, ZINC-FINGER ROTEIN, X-RAV CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKBAMA, GENE REGULATION			MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE
Coumpound		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	KINESIN; CHAIN: NULL;	KINESIN; CHAIN: NULL;	MICKOTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;
SEQFOL D score			58.76			220.57		160.51
PMF		0.99		0.19	-0.02		1.00	
Verify		0.41		0.10	0.03		0.74	
Psi Blast		3.8e-28	. 3.8e-28	0.0022	5.1e-10	6.8e-81	6.80-81	8.5e-69
END		128	130	464	385	352	352	352
STAR		'n	٧.	251	288	_	2	3
CHAI N ID		⋖	⋖					A
PDB		1buo	1buo	1gof	1gof	1bg2	1bg2	1cz7
SEQ No. 19		975	975	526	576	716	116	246

บี≍	CHAI N ID	STAR T AA	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
									MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
٧		2	354	8.5e-69	0.58	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D.	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL
								ú	FROTEIN, NCD CA 131AL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
ш		365	430	5.7e-05	0.21	0.16		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B:	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX, MILTI-SUBINIT
∢		582	766	0.0057	-0.00	0.10		SSOI PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
Ą		_	259	5.2e-72			151.15	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
4		-	259	5.7e-72			151.15	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
٧		2	258	1.2e-55	0.38	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
٧		2	259	5.7e-72	0.45	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
В		272	366	1.7e-17	-0.24	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
M		274	364	1.9e-36	-0.22	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
4		6	352	1.2e-68			157.70	KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
٧		2	346	1.2e-68	0.64	1.00		KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
		4	351	3.4e-66			185.54	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN,

PDB annotation	MOTOR 2 PROTEIN, ATPASE, P- LOOP, MICROTUBULE BINDING PROTEIN	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATFASE, P. LOOP, MCROTUBULE BINDING PROTEIN	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	COMPLEX (BLOOD	COAGULATION/INHIBITOR)	HYDROLASE, SERINE	PROTEINASE), PLASMA CALCIUM	BINDING, 2 GLYCOPROTEIN,	COMPLEX (BLOOD	COAGULATION/INHIBITOR)	COMPLEX (BLOOD	ATTORNOTHROWN IIA:	HYDROLASE, SERINE	PROTEINASE), PLASMA CALCIUM	BINDING, 2 GLYCOPROTEIN,	COMPLEX (BLOOD	COAGULATION/INHIBITOR)	SURFACE PROTEIN MEROZOITE	BLOOD-STAGE EGF-LIKE DOMAIN	EXTRACELLULAR, MODULAR
Coumpound		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	ACTIVATED PROTEIN C;	CHAIN: C, L; D-PHE-PRO-MAI;	Î					ACTIVATED PROTEIN C;	CHAIN: C, L, D-FRE-FRO-MAI;						MEROZOITE SURFACE	(V)	
SEQFOL D score																					
PMF		1.00	0.99	1.00	-0.19							0.41							0.16		
Verify		0.58	-0.10	-0.19	0.03							0.36							-0.11		
Psi Blast		3.4e-66	1.5e-34	le-16	1.5e-10						;	1.1e-24							1.96-20		
END		348	364	366	029							873							820		
STAR T AA		5	276	276	597							745							9		
CHAI N ID			В	æ	Г						1	٦.							<		
PDB ID		3kar	3kin	3kin	laut							lant							loe]		
SEQ OS OS		246	717	226	585						000	786						900	787		

SEQ EI	20 E	CHAI	STAR T AA	END	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
Ö										PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
982	1cki	4	8	107	1.9e-16	0.22	0.17		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR ROTEIN (MCP), VIRUS REGEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPERAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
286	1d4v	¥	556	928	5.7e-09	0.29	-0.12		TNP-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: B; DEATH RECEPTOR 5; CHAIN: A:	APOPTOSIS TRAIL; DRS; LIGAND- RECEPTOR COMPLEX, TRIMERIC JELLY-ROLL, TNF-R 2 SUPERFAMILY, APOPTOSIS
982	Idan	٦	738	823	6.8e-16	0.13	0.11		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE CHLOROMETHYLKETONE	BLOOD COAGULATION, SERINE PROTEASE, COMPACTOR, 2 RECEPTOR BUZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/IGAND)
982	ldan	J	741	831	1.16-24	-0.19	0.27		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOUUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMEITYLKETONE (OFFROMS) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENCYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
982	ldan	1	759	846	3.8e-24	-0.16	0.00		BLOOD COAGULATION FACTOR VIIA; CHAIN: I, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE (DFFRCAMS) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR BUZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
286	Idva	ı	734	831	3.8e-23	-0.18	0.00		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

PDB annotation		HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX	COMPLEMENT INHIBITOR VCP, SP35, COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS	MATRIX PROTEIN EXTRACELJULAR MATRIX, CALCIMA-BINDING, GLYCOROFIEN, ZEREAJ, SIGNAL, MUTIGENE FAMILY, DISEASE MUTATION, 3 EGFLIKE DOMANN, HUMAN PERILLN-1 FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOROTEIN, 2 REPRAT, SIGNAL, MULTIGENE FAMIL Y, DISEASE MUTATION, 3 EGE-LIKE DOMANN, HUANN FIRELLIN-1 FRANKEN, MATRIX PROTEIN	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE
Coumpound	CHAIN); CHAIN: Ľ, M; (DPN)- PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	COMPLEMENT CONTROL PROTEIN; CHAIN: A;	FIBRILIN; CFAIN; NULL;	FIBRILLIN; CHAIN: NULL;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	BLOOD COAGULATION FACTOR VII; CHAIN: A;
SEQFOL D score							
PMF		0.13	0.33	-0.19	90.0	0.01	0.75
Verify		-0.02	0.18	60:00	-0.22	0.07	0.15
Psi Blast		6.8e-16	3.8e-17	1.7e-11	3.46-15	1.9e-10	5.7e-17
END		823	96	337	808	672	181
STAR T AA		738	m	257	738	533	741
CHAI N ID		니	A			A	٧
PDB ID		Idva	leSg	lemn	Iemn	lext	1f7e
SEQ NO: NO:		982	982	982	286	982	982

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PDB annotation	DOMAIN, BLOOD 2 CLOTTING		COMPLEX (BLOOD) COAGULATION/MURIBITOR) COAGULATION/MURIBITOR) CHRISTMAS I SACTOR; COMPLEX, INFIBETOR, HEMOOPHILIARGE; BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCUM- BINDING, HYDROCASE, 3	SERINE PROTEASE FVIJA; BLOOD COAGULATION, SERINE PROTEASE	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35, COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE, PAIR	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE, PLASMA, BLOOD 2 COAGULATION FACTOR	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, PEDERMAL 2 GROWTH FACTOR LIKE DOMAIN
Coumpound		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 11FFHA 11 AVERAGED STRUCTURE) 11FFH4 11FFHA 5	FACTOR TM; CIAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPETIDYL INHIBITOR; CHAIN: C;	VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COAGULATIÓN FACTOR X; CHAIN: NULL;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;
SEQFOL D score							
PMF		0.23	0.11	0.05	-0.09	0.11	-0.13
Verify		0.03	-0.03	0.01	0.18	-0.30	0.04
Psi Blast		9.5e-16	1.3e-32	3.8e-29	1.7e-14	1.16-19	5.1e-10
END		96	840	830	%	814	441
STAR T AA		2	741	741	2	744	369
CHAI N ID			-1	Ţ			T
PDB ID		1hfh	Ipfx	1qfk	Ivvc	lwhe	lxka
SEQ ID NO:		982	982	982	982	982	982

	OR INE AIN		ROTEI APLEX ROTEI	ROTEI MPLEX ROTEI	B1 SEN	B1 SEN	VSTIEM	
tation	ION FACT LOOD TOR, SEF RMAL 2 IKE DOM		/GLYCOP IEIN, COI	/GLYCOP TEIN, COI	DRA, DR HC	DRA, DR HC	LA-DR2, TEIN, SIS, 2	
PDB annotation	AGULAT ACTOR; B TION FAC SE, EPIDE		MBRANE YCOPRO MBRANE	MBRANE YCOPRO MBRANE	(MHC NTIGEN) PLEX (M NTIGEN)	(MHC NTIGEN) IPLEX (M NTIGEN)	YSTEM H ASIC PRO SCLEROS	
	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN		COMPLEX (TRANSMEMBRANE/GLYCOPROTEI N) MHC GLYCOPROTEN, COMPLEX (TRANSMEMBRANE/GLYCOPROTEI	COMPLEX (TRANSMEMBRANE/GLYCOPROTEI N) MHC GLYCOPROTEIN, COMPLEX (TRANSMEMBRANE/GLYCOPROTEI	CÓMPLEX (MHC PROTEIN/ANTIGEN) DRA, DRB1 01010; CÓMPLEX (MHC PROTEIN/ANTIGEN) HISTOCOMPATIBLITY ANTIGEN	COMPLEX (MHC PROTEIN/ANTIGEN) DRA, DRB1 01010; COMPLEX (MHC PROTEIN/ANTIGEN) HSTOCOMPATIEN ITY ANTIGEN	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUITONAMINITY IMMINE SYSTEM	
		PORM						
Coumpound	JLATION HAIN: L,	NEIN NEIN ISC	R: A, B;	IN: A, B;	S II TBILITY IN: A, B, J	S II TBILITY IN: A, B, I	IN: A, D; E; HLA-1	
Com	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	HLA-DR3; CHAIN: A, B; CLIP; CHAIN: C;	HLA-DR3; CHAIN: A, B; CLIP; CHAIN: C;	HLA-DRI CLASS II HISTOCOMPATIBILITY PROTEIN; CHAIN: A, B, D, E, G, H, J, K; HLA-A2; CHAIN: C, F, I, L:	HLA-DRI CLASS II HISTOCOMPATIBILITY PROTEIN: CHAIN: A, B, D, E, G, H, J, K; HLA-A2; CHAIN: C, F, I, L:	HLA-DR2; CHAIN: A, D; HLA- DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	
	PACT	METALLO METALLO II 4MT2 3	HLA-DR3; CHAIN: C;	HLA-DR3; CHAIN: C;	HLA- HISTO PROT H, J, F	HLA- HIST PROT H, I, K	HLA- DR2; CHAI	
SEQFOL D score			61.03		57.96		95.88	
PMF	90:0	0.07		0.39		0.58		
Verify score	0.05	-0.46		-0.06		-0.34		
Psi Blast	1.9e-27	1.4e-09	1.4e-46	1.4e-46	1.4e-46	1.4e-46	8.5e-61	
END	831	617	202	201	201	201	202	
STAR	741	557	22	25	16	\$	ដ	
CHAI N ID	T		æ	m	g	ш	∢	
ED GI	1xka	4mt2	1a6a	Ja6a	laqd	lagd	1bx2	
SEQ No:	286	982	986	986	986	986	986	

PDB annotation	MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM	IMMUNE SYSTEM MHC CLASS II DR2A	IMMUNE SYSTEM MHC CLASS II DR2A	MMUNB SYSTEM RINGS, FILA- DMA; RINGT, HLA-DMB; HISTOCOMPATIBILITY PROTEIN, IMMUNE SYSTEM	HISTOCOMPATIBILITY ANTIGEN I- AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX
Соитроипа	DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	HLA-DR2; CHAIN; A, D; HLA- DR2; CHAIN; B, B; HLA-DR2; CHAIN; C, F;	HLA-DR2; CHAIN: A, D; HLA- DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	MAJOR HISTOCOMPATIBILITY COMPLEX ALPHA CHAIN; COMPLEX ALPHA CHAIN; HISTOCOMPATIBILITY COMPLEX BETA CHAIN; CHAIN; B, MYELLIN BASIC CHAIN; C, FANNE, C, F.	MAJOR HISTOCOMPATIBILITY COMPLEX ALPHA CHAIN; COMPLEX ALPHA CHAIN; CHAIN; A.D. MAJOR HISTOCOMPATIBILITY COMPLEX BETA CHAIN; CHAIN; B.E. MYELLIN BASIC CHAIN; B.E. MYELLIN BASIC FROTEIN; CHAIN; C. F.	CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN: A; CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN: B;	MHC CLASS II I-AK; CHAIN: A, B, P; HEN EGGWHITE LYSOZYME PEPTIDE
SEQFOL D score		59.12				282.05	106.84
PMF			0.46	0.90	0.39		
Verify			-0.39	-0.31	-0.50		
Psi Blast		1.7e-45	1.7e-45	3.4e-60	1.7e-46	3.46-43	10-61
END		204	201	202	201	207	202
STAR		20	45	29	29	20	20
CHAI		g	_α	<	ш	∢	٧
PDB ID		1bx2	1bx2	IfvI	IVI	1hdm	liak
S e S		986	986	986	986	986	986

e e	ANTIGEN I- IY 3 COMPLEX	ANTIGEN I- IY 3 COMPLEX	MHC, FA,	ANTIGEN	ANTIGEN	ANTIGEN	ANTIGEN	ANTIGEN	MHC I-AD	MHC I-AD	MHC I-AD	(UCLEASE) UCLEASE), DROLASE 2 TION, CINE-RICH	X 4), RNA,
PDB annotation	HISTOCOMPATIBILITY ANTIGEN I- AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX	HISTOCOMPATIBILITY ANTIGEN I. AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX	MHC II MHC II, CLASS II MHC, FA, OVALBUMIN PEPTIDE	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN	MHC II MHC II, CLASS II MHC I-AD	MHC II MHC II, CLASS II MHC I-AD	MHC II MHC II, CLASS II MHC I-AD	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (RI-ANG), HYDRO/LASE 2 MOLECULAR RECOGNITION, BETTOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,				
Coumpound	MHC CLASS II I-AK; CHAIN: A, B, P; HEN EGGWHITE LYSOZYME PEPTIDE	MHC CLASS II I-AK; CHAIN; A, B, P; HEN EGGWHITE LYSOZYME PEPTIDE	MHC CLASS II I-AD; CHAIN: A, B;	MHC CLASS II I-EK; CHAIN: A, B, C, D;	MHC CLASS II I-EK; CHAIN: A, B, C, D;	MHC CLASS II I-EK; CHAIN: A, B, C, D;	MHC CLASS II I-EK; CHAIN: A, B, C, D;	MHC CLASS II I-EK; CHAIN: A, B, C, D;	MHC CLASS II I-AD; CHAIN: A, B;	MHC CLASS II I-AD; CHAIN: A, B;	MHC CLASS II I-AD; CHAIN: A, B;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;
SEQFOL D score		59.46	58.50	100.86		53.16	58.75		109.34		59.80		
PMF	1:00				0.95			0.21		1.00		0.60	68.0
Verify	-0.12				-0.28			-0.34		60.0		-0.43	-0.29
Psi Blast	Ie-61	1.5e-43	1.2e-43	5.16-59	5,1e-59	3.4c-45	3,4e-45	3.4e-45	3,4e-61	3.4e-6I	3.4e-44	1.9e-11	3.8e-15
END	202	201	201	203	203	661	199	199	207	206	201	214	130
STAR T AA	37	23	_	21	27	2	-	51	20	37	2	52	49
CHAI	A	m	m	٧	٧	В	В	В	Ą	A	м	. 4	¥.
70B CI	liak	liak	liao	liea	liea	liea	lieb	lieb	2iad	Ziad	Ziad	la4y	la9n
S e S	986	986	986	986	986	986	986	986	986	986	986	284	987

	_							_	_									_	
PDB annotation	SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX	(NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL	ALPHA-HELICAL, CONTRACTILE PROTEIN	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL	STRUCTURE, RAB	GERANYLGERANYLTRANSFERASE,	2.0 A 2 RESOLUTION, N-	SUBUNIT, BETA SUBUNIT	Section 4 Court in the Court of Section 1 1 Section 1	CONTRACTILE PROTEIN LEUCINE-	CYLINDER, DYNEIN, 2	CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE-	RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2
Coumpound		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B";	CHAIN: B, D;	TROPOMYOSIN; CHAIN: A, B, C, D		INTERNALIN B; CHAIN: A;	RAB	GERANYLGERANYLTRANSFE	RASE ALPHA SUBUNIT;	CHAIN: A, C; RAB	RASE BETA SUBUNIT; CHAIN:	B, D;	OUTEK AKM DYNEIN; CHAIN:	433		OUTER ARM DYNEIN; CHAIN:	¥;
SEQFOL D score																			
PMF		0.40	0.94	0.35		0.03		0.98	99.0					9	75.0			0.55	
Verify		0.10	0.07	0.05		-0.72		0.33	0.27					0,0	-0.19			80.0-	
Psi Blast		3.8e-14	3.8e-15	5.7e-14		5.1e-19		1.2e-18	1.2e-14					1	4			3.8e-15	
END		199	145	661		493		162	151					9	2			155	
STAR T AA		52	49	52		231		2	34					9	ę			50	
CHAI		¥	o	၁		<		٧	Ą						<			<	
PDB ID		la9n	la9n	la9n		lclg		q0p1	1dcc					9	Spi			lds9	
SEQ No.		186	786	287		284		186	286					100	9			282	

PDB annotation	CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN TRIPLE- HELIX COLLED COIL, CONTRACTILE PROTEIN	CITA-ASEA-CITYA-TINA GRACIA-P. CITA-ASEA-CITYA-TINA GRACIA-P. RROTBIN GAP, RAVIP, LANGAP, LRAL ELGUNE-2 RICH REPRA-I FROMEN, PROFEN, PRANTER, PROFEN, PROFENDA, TWINNING, REMIREDSA, TWINNING, REMOREDRA, TWINNING, MRROGERICAL TWINNING,		TRANSFERASE CASEIN KINASE BETA SUBUNIT (1-182), SER/THR PROTEIN KINASE, 2 ZN FINGER	TRANSFERASE CASEIN KINASE BETA SUBUNIT (1-182), SER/THR PROTEIN KINASE, 2 ZN FINGER	OXIDOREDICTASE PERROCYTOCHROME C-OXYGEN OXIDOREDICTASE; OXIDOREDICTASE; CYTOCHROME (C)-OXYGEN CYTOCHROME (C)-OXYGEN	TRANSCRIPTION TRANSFERASE, TRANSCRIPTION, DNA-DIRECTED TRANSCRIPTION, DNA-DIRECTED STRUCTURE
	CHI	S # S	TRA GTP FOR PRO LRR PRO HEN MER	_	TRA PRO	TRA BET PRO		
Coumpound	H 1001D & TATIO HAND INVANIA	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	GTPASE-ACHVATING PROTEIN RNAL_SCEPO; CHAIN: A, B;		CASEIN KINASE II; CHAIN: A, B;	CASEIN KINASE II; CHAIN: A, B;	CYTOCHROMB C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q	DNA-DIRECTED RNA POLYMERASIS, CHAIN: A, B; DNA-DIRECTED RNA POLYMERASIS; CHAIN: G; DNA- DIRECTED RNA POLYMERASIS; CHAIN: D; DNA-DIRECTED
SEQFOL D score	7.5 04	72.54						
PMF			0.13		1.00	1.00	0.07	0.96
Verify score			-0.14		0.46	0.46	0.10	-0.22
Psi Blast	7.60.07	/.pe-0./	1.96-12		3.8e-56	6.8e-51	8.5e-29	0
END	101	164	210		123	123	141	1076
STAR T AA	260	730	57		7	7	73	_
CHAI N ID		<	4		A	4	н	၁
PDB	-	ndbr	lyrg		1qf8	14f8	2000	1ddq
SEQ O O	200	/86	987		166	166	993	994

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PDB annotation		TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION			LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITM, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITN, B3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,	ZINC-BINDING PROTEIN ZINC- BINDING PROTEIN, XNF7, BBOX, DEVEL OPMENT, 3 MID-BLASTULA- TRANSITION	METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING FINGER (C3HC4)	DAY DEPONDED WEST
Coumpound	RNA POLYMERASE; CHAIN: E;	TRANSCRIPTION FACTOR PML; CHAIN: NULL;	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	SIGNAL TRANSDUCTION PROTEIN CBL, CHAIN: A; ZAP- 70 PEPTIDB, CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBGCF; CHAIN: C;	SIGNAL TRANSDUCTION PROTEIN CBI, CHAIN: A; ZAP- 70 PEPTIDE, CHAIN: B; UBIQUITIN-CONJUGATING EINZ'ME EI2-18 KDA UBCH7; CHAIN: C,	NUCLEAR FACTOR XNF7; CHAIN: NULL;	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI; CHAIN: A:	DACT. CHAIN, MILL I.
SEQFOL D score									
PMF		0.05	0.59	0.47	0.52	0.30	0.03	0.46	070
Verify		-0.39	0.29	-0.45	-0.04	-0.46	-0.11	-0.33	0.13
Psi Blast		1.4e-08	1.7e-12	5.7e-12	5.1e-10	3.8c-09	3.4e-05	0.00017	1 16.16
END AA		20	51	09	51	09	134	25	100
STAR T AA		2	10	9	10	6	86	9	4
CHAI N ID					4	⋖		<	
PDB		lbor	lche	1che	1fbv	1fbv	1fre	1g25	lrmd
SEQ ID NO:		566	995	995	995	995	995	995	995

		_					_	_						_	_	_	_	_	_				
PDB annotation	RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FROER, 2 ZNC BRUCKER, 2 ZNC BRUCKER, CINSTER, ZNC FINGER, DNA-BINDING PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) SREBP-1A; STEROL REGULATORY ELEMENT	BINDING PROTEIN, 2 BASIC-HELIX-	LOOP-HELIX-LEUCINE ZIPPER, SRERP TRANSCRIPTION 3 RACTOR	COMPLEX (TRANSCRIPTION	COMPLEX (DNA-BINDING	PROTEIN/DNA) MYN PROTEIN;	MAX, DNA BINDING, BASIC-HELIX- 1 OOP-HET IX-1 BTICINE 2199BB 3	TRANSCRIPTION FACTOR	COMPLEX (DNA-BINDING	PROTEIN/DNA)	COMPLEX (TRANSCRIPTION	FACTOR MAX/DNA)	TRANSCRIPTIONAL REGULATION,	DNA BINDING, COMPLEX 2	(TRANSCRIPTION FACTOR	MAX/DNA)	COMPLEX (TRANSCRIPTION	FACTOR MAX/DNA)	TRANSCRIPTIONAL REGULATION,	DNA BINDING, COMPLEX 2	(TRANSCRIPTION FACTOR MAX/DNA)
Coumpound		STEROL REGULATORY	ELEMENT BINDING PROTEIN 1A; CHAIN: A. B. C. D: DNA:	CHAIN: E, F, G, H;			MAX PROTEIN: CHAIN: A. C:	DNA; CHAIN: B, D;					TRANSCRIPTION FACTOR	MAX; CHAIN: A, B; DNA (5'-	D(*CP*AP*CP*CP*AP*CP*GP*T	P*GP*GP*T)-3', CHAIN: C, D;			TRANSCRIPTION FACTOR	MAX; CHAIN: A, B; DNA (5'-	D(*CP*AP*CP*CP*AP*CP*GP*T	P*GP*GP*T)-3', CHAIN: C, D;	
SEQFOL D score																							
PMF		0.01					0.01						0.10						0.19				
Verify		-0.25					-0.60						-0.26						-0.32				
Psi Blast		7.6e-09					3.8e-15						1.9e-13						1.9e-12				
END		345					354						343						343				
STAR		277					277						568						277				
CHAI		m					٧						∢.						м				
PDB ID		lam9					1an2						lhio						lhlo				
SEQ NO:		966					966						966						986				

	EDB ED	CHAI N ID	STAR	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
-	16yu	⋖	17	139	5.1e-46	-0.02	0.64		GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT,
	1byu	m	13	139	1.2e-46	0.17	0.72		GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN TRANSPORT
	lec0	∢ .	23	140	3.4e-47	-0.23	0.96		TRANSFORMING PROTEIN RHOA; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA: CHAIN: F. F.	SIGNATUR PROTEIN GIP-BINDING PROTEIN RHOA, GTPASE RHOA; RHO GDI I; RHO GTPASE, G-
	lexz	۷	23	140	le-47	-0.14	86.0		HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A: PKN: CHAIN: B:	SIGNALING PROTEIN PROTEIN- PROTEIN COMPLEX, ANTIPARALLE, COLLED-COLL.
	1d5c	∢	22	143	1.4e-49	0.14	0.84		RAB6 GIPASE; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G- PROTEIN, GTPASE, RAB6, VESICULAR TRAPPICKING
	1ds6	⋖	ដ	140	8.5e-49	-0.05	0.88		RAS-REI-ATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;	SIGNALIMO PROTEIN P21-R-ACZ: RHO GDI 2, RHO-GDI BETA, LY-GDI; BETA SANDWHIGH; PROTEIN: PROTEIN COMPLEX, CADOMAIN, 2 IMAUNOGLOBULIN POLD, WALKER FOLD, GTP-BINDING
	libr	₹	70	145	1.4e-45			68.78	RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GIPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NICLEAR TRANSPORT RECEPTOR
	ImhI		17	145	5.1e-50			52,24	RACI; CHAIN: NUIL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY: RAS SUPER 2 FAMILY
	ImhI		22	140	5,1e-50	-0.12	0.87		RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
	lrrp	С	19	145	1.4e-45			65.13	RAN; CHAIN: A, C; NUCLEAR	COMPLEX (SMALL

PDB annotation	GTPASEANUCLEAR PROTEIN) COMPLEX (SMALL GPASEANUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT	COMPLEX (GTP. BINDINGEFERCOR) RAS-RELATED PROTEIN RABSA, COMPLEX (GTP. BINDINGEFERCOR), OR PROTEIN, EFECTOR, RABCOR, 2 SYNAPTIC EXOCYTORSI, RAB PROTEIN, RABSA, RABPHILIN	COMPLEX (GIP. BRUDINGEREECTOR) RAS.RELATED PROTEIN RABSA, COMPLEX (GIP. BRUDINGEREECTOR), OR ROLEIN, EFECTOR, RABCOR, 2 SYNAPHIC EXOCYTORSI, RAB PROTEIN, RABPILLIN	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3. HYDROLASE	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
Coumpound	PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	RAB3A; CHAIN: A;	RAB3A; CHAIN: A;
SEQFOL D score		54.15				11.79
PMF			0.78	0.89	0.88	
Verify score			0.17	-0.07	0.19	
Psi Blast		1.7e-53	1.70-53	3.40-46	5.10-55	5.1e-55
END		144	143	141	143	145
STAR T AA		17	18	22	11	17
CHAI N ID		∢	¥	Ą	<	4
PDB ID		1zbd	1zbd	2ngr	3rab	3rab
SEQ NO ES		766	997	266	997	. 166

	,				OMAIN, MENT,	N. N.	ř S	
PDB annotation	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN				TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	KINASE KINASE, TWITCHIN INTRASTERIC REGULATION	KINASE RABBIT MUSCLE
Coumpound	CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE; CHAIN: NULL;	TRANSEREASEPHORMAN NSFREASE) SCAARPS DEBENDENT FORTEN KINASE (C.C.2.1.37) SCARSE) IA-BA ISOBAZTIBE MUTANT WITH SER 139 IAPAL REPLACED BY AL (NSIASO COMPLEX WITH THE PRETIDE IAPAL PHERITOE IAPAL NEHRIPORE AREA SEASON THE DETERGENT MIGGAS IAPAL E	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK 3 (E.C.2.7.1.37) ICMK 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP- DEPENDBOT PROTEIN KINASE (B.C.2.7.1.37) (CARV) LCTP 3 (CATALYTIC SUBUNIT) LCTP 4	SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE- PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TWITCHIN; CHAIN: NULL;	TWITCHIN; CHAIN: A, B;	PHOSPHORYLASE KINASE;
SEQFOL D score								
PMF	0.16	0.53	0.47	0.78	0.51	0.37	0.72	08.0
Verify	-0.20	-0.21	-0.17	-0.02	-0.02	-0.02	-0.02	0.13
Psi Blast	1.7e-50	5.1e-66	5.1e-66	1.2e-60	3,4e-53	1.2e-38	1.2e-40	3.4e-54
END	174	175	175	191	091	691	691	140
STAR	-		_	_	-	_	-	_
CHAI N ID		Д	ш	13	2		¥	
EDB ID	1a06	lapm	lcmk	lctp	115m	lkoa	1kob	1phk
SEQ NO DE	866	866	866	866	866	866	866	866

							1	1	7
PDB annotation	GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINFIBITION	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	CELL ADHESION NEURAL CELL ADHESION	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FOF, FGPR, IMMUNOGLOBUIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH	TACTOR KACLETOR GROWTH FACTORGROWTH FACTOR RECEPTOR FOF, FGFR, IMAUNOGLOBULIN-LIKE, SIGNE, TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTORGROWTH	GROWTH FACTOR/GROWTH PACTOR RECEPTOR FOF, FORTA IMMUNOGI.OBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	CELL ADHESION NCAM; NCAM,
Соитроии		TITIN; CHAIN: A, B;	TITIN; CHAIN: A, B;	HEMOLIN; CHAIN: A, B;	AXONIN-1; CHAIN: A;	FIBROBLAST GROWTH PACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FIBROBLAST GROWTH C, D;	FIBROBLAST GROWTH FACTOR 2: CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2, CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	NEURAL CELL ADHESION
SEQFOL D score									
PMF		0.75	0.25	0.40	0.10	0.15	0.21	-0.03	-0.13
Verify		0.18	-0.12	0.28	60.0	0.08	0.15	0.03	0.11
Psi Blast		1.7e-34	1.9e-34	1.7e-27	3.4e-34	3.4e-25	5.1e-36	1.2e-26	3.4e-18
END AA		149	186	283	283	661	284	199	282
STAR T AA		-	_	10	29	21	112	21	123
CHAI N ID		V	∢	¥	٧	ပ	Q	D	Ą
EDB CI		1tki	1tki	19ih	1cs6	lcvs	lcvs .	lovs	lepf
SEQ NO:		866	866	1000	1000	1000	1000	0001	1000

SEQ El S	EDB CII	CHAI N ID	STAR	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
									MOLECULE; CHAIN: A, B, C, D;	IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
0001	lepf	∢	33	201	3.4e-24	0.11	-0.09		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1000	PZI	A	1117	281	1.7e-19	0.12	0.31		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN
1000	1224	V	28	208	3.4e-28	0.00	0.22		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI- ALPHA: IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN
1000	1f6a	< -	116	281	Ie-17	15.0	0.57		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN; A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	MAMUNE SYSTEM HIGH AFFINITY (GB-FC RECEPPOL, PCERSILON) (GB-FC MAMUNGGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE BINDING 2 PROTEIN, IGE ANTRODY, IGE-FC
1000	1f6a	4	26	207	1.4e-27	-0.04	0.12		HIGH AFFINITY INMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; 10 EPSILON CHAIN C REGION; CHAIN: B, D;	MAMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FCGESELON) IGE-FC, IMMUNGOLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1000	Ifeg	V V	115	281	1.7e-19	0.15	-0.12		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32
1000	lfcg	A	26	205	5.1e-29	0.23	0.41		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32
1000	1fnl	V	114	281	3.4e-17	0.05	90.0		LOW AFFINITY	IMMUNE SYSTEM RECEPTOR BETA

PDB annotation	SANDWICH, IMMUNOGLOBULIN- LIKE, RECEPTOR	IMMUNE SYSTEM RECEPTOR BETA	SANDWICH, IMMUNOGLOBULIN- LIKE, RECEPTOR	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	MUSCLE PROTEIN CONNECTIN,	NEXTM5; CELL ADHESION,	GLYCOPROTEIN,	TRANSMEMBRANE, REPEAT,	BRAIN, 2 IMMUNOGLOBULIN FOLD,	ALTERNATIVE SPLICING, SIGNAL, 3	MUSCLE PROTEIN	CELL INHIBITORY RECEPTOR:	INHIBITORY RECEPTOR, NATURAL	KILLER CELLS, IMMUNOLOGICAL 2	RECEPTORS, IMMUNOGLOBULIN	FOLD	INHIBITORY RECEPTOR KILLER	CELL INHIBITORY RECEPTOR;	INHIBITORY RECEPTOR, NATURAL	KILLER CELLS, IMMUNOLOGICAL 2	RECEPTORS, IMMUNOGLOBULIN FOLD	INHIBITORY RECEPTOR KILLER	CELL INHIBITORY RECEPTOR;	INHIBITORY RECEPTOR, NATURAL	KILLER CELLS, IMMUNOLOGICAL 2	RECEPTORS, IMMUNOGLOBULIN	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR:
Coumpound	IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	LOW AFFINITY	IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	TWITCHIN; CHAIN: NULL;	TITIN; CHAIN: NULL;						nes de lo min del nes de la	F38-CE42 KIK; CHAIN: NOLE;					P58-CL42 KIR; CHAIN: NULL;					P58-CL42 KIR; CHAIN: NULL;					P58-CL42 KIR; CHAIN: NULL;
SEQFOL D score						_		-														71.59					
PMF		0.58		0.33	-0.15						100	9/:0					0.22							_			0.87
Verify		0.07		0.35	0.47	-					00.0	07:0					-0.51										0.22
Psi Blast		1.5e-24		5.1e-12	3.46-13						00.7	67-24:0					6.8e-13					1e-30					1e-30
END		206		284	284						000	707					113					216					204
STAR T AA		24		207	213) II					12					27					28
CHAI		A	,																								
PDB		1fh1		Ikoa	Inct						1	T I					lnkr					inkr					lnkr
SEQ NO:		1000		1000	1000						1000	3					000					1000					1000

PDB annotation	INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD		IMMUNOGLOBULIN ANTI- NITROPHENOL, LAMBDA LIGHT CHAIN, IMMUNOGLOBULIN	IMMUNE SYSTEM PS8 NATURAL KILLER CELL RECEPTOR, KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLÓBULIN	IMMUNE SYSTEM PS8 NATURAL KILLER CELL RECEPTOR, KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, IMMUNOGLOBULIN	IMMUNE SYSTEM CD32; RECEPTOR, PC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, PC, CD32, IMMUNE SYSTEM	HYDROLASE C2 DOMAIN, PHOSPHOTIDYLINOSITOL, PHOSPHOTASE, HYDROLASE	HYDROLASE C2 DOMAIN, PHOSPHOTIDYLINOSITOL, PHOSPHOTASE, HYDROLASE
Coumpound	-	MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	FAB FRAGMENT; CHAIN: NULL;	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIB; CHAIN: A;	PHOSPHOINOSITIDE PHOSPHOTASE PTEN; CHAIN: A;	PHOSPHOINOSITIDE PHOSPHOTASE PTEN; CHAIN: A;
SEQFOL D score			54.09						
PMF		-0.18		0.51	0.74	-0.08	0.55	0.07	0.07
Verify		0.37		0.22	0.23	0.26	0.03	-0.64	-0.64
Psi Blast		3.4e-13	8.5e-07	3.46-29	5.1e-29	5.1e-20	3,4e-29	0.0019	0.0019
END AA		284	236	282	203	281	506	344	262
STAR T AA		213	28	1117	36	115	26	162	209
CHAI N ID			Ξ	¥.	A	¥	¥.	∢ .	٧
PDB ID		Itnm	lyuh	2dli	2dli	2feb	2fcb	1d5r	1d5r
SEQ ID NO:		1000	1000	0001	1000	1000	1000	1001	1003

PDB annotation	Tarrest of the state of the sta	HYDROLASE CZ DOMAIN, PHOSPHOTIDYLINOSITOL, PHOSPHOTASE, HYDROLASE	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN AT PHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COLLED-COLLS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	TANDEM 2 DELIVER RECION, 2.2	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	ENDOCYTOSIS/EXOCYTOSIS	NSEC1; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	COMPLEX (DNA-BINDING	PROTEIN/DNA) TUS; TER; DNA-	BINDING, DNA REPLICATION, 2	COMPLEX (DNA-BINDING	PROTEIN/DNA)	MEMBRANE PROTEIN FOUR HELIX	BUNDLE, ALPHA HELIX	MEMBRANE PROTEIN FOUR HELIX	CONTRACTIF R PROTEIN TOBER	HELLY COILED COIL,
Coumpound	DOMESTIC OF STREET	PHOSPHOINGSTIDE PHOSPHOTASE PTEN; CHAIN: A;	ALPHA SPECTRIN; CHAIN: A,	S. C.		ALPHA SPECTRIN; CHAIN: A,	B, C;			ALPHA SPECTRIN; CHAIN: A,	B, C;				SYNTAXIN BINDING PROTEIN	I; CHAIN: A; SYNTAXIN IA;	CHAIN: B;	REPLICATION TERMINATOR	PROTEIN; CHAIN: A; DNA	6MER DUPLEX REPLICATION	TERMINATOR; CHAIN: B, C;		SSOI PROTEIN; CHAIN: A;		SSOI PROTEIN; CHAIN: A;	HIMAN SKELFTAL MUSCUE	ALPHA-ACTININ 2; CHAIN: A;
SEQFOL D score																											
PMF	200	0.07	-0.03			0.13				0.23					10.0			0.00					0.00		-0.12	0.05	3
Verify score	0.04	-0.64	0.04			-0.08				-0.12					-0.32			-0.61					0.00	or or the delices of the same	0.02	-0.31	
Psi Blast	0,000	0.0019	5.7e-16			1.5e-16				1.7e-13					5.7c-18			0.0013					3.8e-11		7.6e-II	1 le-22	
END AA	244	344	396			429				505					470			288					329		40I	370	
STAR T AA	100	167	<u>1</u> 5			213				293					236			19					I33		217	7.5	:
CHAI N ID		V.	¥			٧				<					ш			√.		_			¥		<	V	
PDB ID	176	icei	Icun			Icun				Icun					Idni			lecr					1E0		Ifio	Ionn	
SEQ No: D	1004	±01	0101			1010				1010					1010			1010					1010		1010	1010	

PDB annotation	CONTRACTILE PROTEIN					TRANSMEMBRANE PROTEIN	COLICIN, BACTERIOCIN, ION	CHANNEL FORMATION, IRANSMEMBRANE 2 PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	Other Land on a 14 minor rather
	CONTRACT					TRANSMER	COLICIN, B	TRANSME	STRUCTUR	REPEATSC	HELICAL L	TANDEM 3	STRUCTUR	STRUCTUR	REPEATS	HELICAL L	TANDEM 3	STRUCTUR	STRUCTUR	REPEATS	HELICALL	TANDEM 3	STRUCTUR	STRUCTUR	REPEATS	HELICALL	TANDEM 3	STRUCTUR	COLUMN TO SERVICE SERV
Coumpound		C OUR AND A SECURITION OF SECU	IDFN 3	DEFENSIN DEFENSIN /HNP\$-3 1DFN 3	DEFENSIN DEFENSIN /HNPS-3 1DFN 3	COLICIN IA; CHAIN: NULL;			ALPHA SPECTRIN; CHAIN: A,	B, C;				ALPHA SPECTRIN; CHAIN: A,	B, C;				ALPHA SPECTRIN; CHAIN: A,	B, C;				ALPHA SPECTRIN; CHAIN: A,	B, C;				1 THE PART COMPONENT AND A
SEQFOL D score		20.02	16:60			148.75																							
PMF				1.00	1.00				-0.09					0.17					0.04					-0.02					000
Verify				-0.35	-0.35				0.12					90'0					0.11					0.44					000
Psi Blast			71-91-1	1.1e-12	3.4e-11	5.7e-59			3.8e-15					1.9e-15					3.8e-21					1.9e-19					1 00 00
END		95	92	138	138	989			394					447					583					634					284
STAR		90.	109	110	110	14			190					218					345					419					9
CHAI			₹ .	∢	¥				4					4					¥					٧					<
PDB		27.0	IIII	Idfi	1dfn	1cii			lcun					Icun					lcun					lcnn					lann
SEQ EQ		0101	CIO	1013	1013	1014			1014					1014					1014					1014					1014

PDB annotation	REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COLIED-COILS, STRUCTURAL PROTEIN	SIGNALING PROTEIN GUANINE NUCLECHINE, BINDING PROTEIN I; GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2. RELATED, LARGE GTRASE FAMILY, SIGNALING PROTEIN	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	CHAPERONE ARCHAEAL PROTEIN	CHAPERONE ARCHAEAL PROTEIN	CHAPERONE ARCHAEAL PROTEIN
Coumpound	B, C;	ALPHA SPECTRIN; CHAIN: A, B, C;	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN I; CHAIN: A;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	SSO1 PROTEIN; CHAIN: A;	PREFOLDIN; CHAIN; A; PREFOLDIN; CHAIN; B; PREFOLDIN; CHAIN; C;	PREFOLDIN; CHAIN; A; PREFOLDIN; CHAIN; B; PREFOLDIN; CHAIN; C;	PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B;
SEQFOL D score										
PMF		0.12	0.17	-0.07	0.23	0.66	-0.17	0.01	0.15	0.22
Verify		-0.06	-0.16	0.07	-0.04	0.02	10.0	80.0	0.00	0.26
Psi Blast		5.7e-10	0.0057	1.5e-18	5.7e-26	1.7e-09	1.9e-11	1.9e-05	3.8e-07	1.9e-05
END		741	307	509	865	733	518	422	513	578
STAR T AA		525	55	297	370	484	361	308	391	472
CHAI N ID		¥	∢	æ	en en	В	<	o	၁	C
PDB ID		Icun	1483	1dh1	Idn1	1dn1	1fio	1fxk	1fxk	1fxk
SEQ No.		1014	1014	1014	1014	1014	1014	1014	1014	1014
	PDB CHAI STAR END Psi Biast Verify PMF SEQFOL Coumpound 1D N ID T AA AA AA seore seore D seore	PDB CIAAI STAR END P4 Bhat Verify PMF SRQFOL Coumpound 1D N1D TAA AA Assore score D score B.C.	PDB CIGAI STAR END P4 Blast Verify PAIF SRQPOL Coumpound	PB GIAA STAR EMD F4 Blist Verify Pape Store Disore Disor	PB GIAA STAR END F4 Blast Seere Seere Description Seere Description Seere Description Seere Seere Description Seere Seere Description Seere See	PB GIAA STAR END F4 Blist Verify PMF SROPOL Coumpound	PB GIAA STAR END F4 Blist Seore Disore Disore	PB GIAA STAR END F4 Blast Seore Seore Descret B. C.	PB GIAA STAR END F4 Blist Verify PMF SROPOL Coumpound	PB GIAA STAR END F4 Blast Verify Fort Store Disore B. C.

PDB annotation		CHAPERONE ARCHAEAL PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELLX COLLED COLL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COLLED COIL, CONTRACTILE PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA)
Coumpound	PREFOLDIN; CHAIN: C;	PREFOLDIN, CHAIN: A; PREFOLDIN, CHAIN: B; PREFOLDIN, CHAIN: C;	HUMAN SKELETAL MÜSCLE ALPHA-ACTININ 2; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;			
SEQFOL D score											
PMF		0.11	0.07	0.01	0.15	0.03	0.03	0.62	90:0-	0.03	0.28
Verify		0.21	0.15	0.48	0.20	-0.05	-0.06	-0.31	0.01	0.11	-0.37
Psi Blast		0.00057	1.16-24	1.3e-32	7.6e-27	3.8e-17	3.8e-15	1.2e-23	1.7e-24	1.7e-26	1e-27
END		635	549	280	030	746	398	429	468	498	555
STAR		552	272	321	359	471	81	349	378	405	472
CHAI		၁	A	4	4	A	A	A	¥	٧	⋖
PDB		1fxk	lquu	Iquu	Impi	lquu	lquu	laih	lalh	laih	lalh
SEQ ID NO:		1014	1014	1014	1014	1014	1014	1015	1015	1015	1015

			1					_
PDB annotation	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN		COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA THYBRACTON, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA FINGERCTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA
Coumpound	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	OGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	DNA-BINDING PROTEIN HUMAN ENIANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 11 IBBO 3 REPLACED BY ABU (CILABU) (MMR, 60 STRUCTURES) 1BBO	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER
SEQFOL D score								
PMF		0.10	0.87	0.18	0.81	0.72	0.82	9.95
Verify score		0.34	0.10	-0.65	-0.12	-0.01	-0.01	-0.25
Psi Blast		3.4e-30	3.4e-30	1.76-10	1.7e-41	L.7e-42	1.7e-45	5.1e-47
END		186	0101	554	429	468	496	527
STAR T AA		901	675	505	349	374	404	443
CHAI N ID		¥	∢		U	o	ပ	0
EDB EDB		lalh	Iath	1bbo	Imey	1mey	Imey	Imey
SEQ ID NO:		1015	1015	1015	1015	1015	1015	1015

nd PDB annotation	C. F. G; INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	D, E; COMPLEX (ZINC FINGER/DNA) ZINC FINGER PROTEIN, DNA			FINGER FINGER, PROTEIN-DNA			_		CRYSTAL STRUCTURE, COMPLEX					CRYSTAL STRUCTURE, COMPLEX					CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)				CRYSTAL STRUCTURE, COMPLEX	
Coumpound	PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E;	PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	ricolitate, crimina	DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN; C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		
SEQFOL D score																										
PMF		0.90		-0.14			-0.20					-0.15					0.51					98.0				
Verify score		-0.26		0.01			0.02					0.12					0.25					-0.07				
Psi Blast		3.4e-46		1.5e-36			6.8e-44					5.1e-45					3.4e-50					3.4e-50	_			
END		929		612			778				1	953				.00	186					1010				
STAR T AA		471		530			869					840				,	35					878				
CHAI N ID		ပ		ပ			ပ					O				,	ు					၁				
PDB CI		lmey		Imey			Imey				J	Imey				J.	Imey					1mey				_
SEQ NO ID		1015		1015			1015					1015			_	,	CIOI					1015				_

PDB annotation	R FINGER, PROTEIN-DNA NTERACTION, RYOTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	-		
Coumpound	CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN; A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN; C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TRANSCRIPTION REGULATION YEART TRANSCRIPTION PEGULATION PACTOR ADRI (RESIDUES 130 - 135) IPAA 5 (PARA - CARBOXY TEMINAL ZING FINGER DAMAN) MUTARY WITH IPAA 4 PRO 131 REPLACED BY ALA, WE 131 REPLACED
SEQFOL D score						
PMF		0.24	-0.18	0.42	0.65	96:0
Verify		-0.71	0.22	-0.03	0.23	-0.38
Psi Blast		5.1e-11	1.56-11	1e-12	8.5e-12	1.7e-05
END		556	865	953	1010	1013
STAR T AA		528	839	926	982	586
CHAI		o	o	₀	Ð	
PDB		Imey	Imey	Imey	lmey	Ipaa
SEQ No.		1015	1015	1015	1015	1015

	ZINC FINGER TRANSCRIPTION FACTOR SPI; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION; SP1	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S	GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE. DNA BINDING PROTEIN.	ZINC FINGER, COMPLEX 3	REGULATION/DNA)	COMPLEX (TRANSCRIPTION PEGIII ATTOM/DNA) TEITA - 55	GENE; NMR, TFIIIA, PROTEIN, DNA,	TRANSCRIPTION FACTOR, 5S RNA 2 GENE DNA BINDING DEOTEIN	ZINC FINGER, COMPLEX 3	(TRANSCRIPTION	COMPLEX (TRANSCRIPTION	REGULATION/DNA) TFIIIA; 5S	GENE; NMR, TFIIIA, PROTEIN, DNA,	GENE DNA BRIDING PROTEIN	ZINC FINGER, COMPLEX 3	(TRANSCRIPTION REGULATION/DNA)
(NMR, 10 STRUCTURES) 1PAA 6	SP1F3; CHAIN: NULL;	SP1F2; CHAIN: NULL;	SP1F2; CHAIN: NULL;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE;	CHAIN: E, F,			TRANSCRIPTION FACTOR IIIA; CHAIN: A: 5S RNA GENE:	CHAIN: E, F;				TRANSCRIPTION FACTOR IIIA:	CHAIN: A; 5S RNA GENE;	CHAIN: E, F,			
	0.70	0.27	0.90	0.05				0.23					0.03					
	-0.10	-0.77	-0.54	-0.11				0.15					-0.17					
	0.00051	0.00017	1.9e-05	6.8e-17				3.4e-18					1.7e-18					
	1010	375	1010	468				496					551					
	586	349	586	377				405					472					
				¥			.	. V					A					
	1sp1	lsp2	1sp2	III3				1163					1163		-			
	1015	1015	1015	1015				1015					1015					
	(NMR, 10 STRUCTURES) 1PAA 6	14p1 985 1010 0.00051 -0.10 0.70 SP1P3; CHAIN: NULL; 2	18p1 985 1010 0.00031 -0.10 0.70 SP.1P3; CHAIN; NULL; 2 18p2 349 375 0.00017 -0.77 0.27 SP.1P2; CHAIN; NULL; 2 1 1 1 1 1 1 1 1 1	Isp1 985 1010 0.00051 -0.10 0.70 RP.193 CHAIN.NULL; 2 Isp2 349 375 0.00017 -0.77 0.27 SP.1P3 CHAIN.NULL; 2 Isp2 985 1010 I.9e-05 -0.54 0.59 SP.1P2 CHAIN.NULL; 2 1sp2 985 1010 I.9e-05 -0.54 0.59 SP.1P2 CHAIN.NULL; 2	15p1 985 1010 0.00051 -0.10 0.70 SP1P3; CHAIN: NULL; 15p2 349 375 0.00017 -0.77 0.27 SP1P2; CHAIN: NULL; 15p2 985 1010 1.9e-05 -0.54 0.90 SP1P2; CHAIN: NULL; 14p3 468 6.8e-17 -0.11 0.05 TRANSCRPTIONFACTOR IIIA; 14p3 A 377 468 6.8e-17 -0.11 0.05 TRANSCRPTIONFACTOR IIIA; 14p3 A 377 468 6.8e-17 -0.11 0.05 CHAIN: 3,5 SRNA GENE;	18p1 985 1010 0.00051 -0.10 0.70 SP.1P3; CHAIN: NULL; 18p2 339 375 0.00017 -0.77 0.27 SP.1P3; CHAIN: NULL; 18p2 18s2 1010 1.9e-0.5 0.54 0.59 SP.1P2; CHAIN: NULL; 18p2 18s2 1010 1.5e-0.5 0.54 0.59 SP.1P2; CHAIN: NULL; 18p2 18p3 18p3	18p2 349 375 0.000 0.000 0.70 SP. 1P3; CHAIN: NULL; 18p2 1319 375 0.000 17 0.27 SP. 1P3; CHAIN: NULL; 18p2 18p	18p2 316 0.00031 0.10 0.70 SPIECTURES) IPAA 6 18p2 316 0.00017 0.77 0.27 SPIECTURE) IPAA 6 18p2 319 375 0.00017 0.27 0.27 SPIECTURE) IPAL 1 18p2 985 1010 1.9e-05 0.54 0.90 SPIECTURE IPACTOR IIIA; 18p3 377 468 6.8e-17 0.11 0.05 TRANSCEPTON FACTOR IIIA; CHARK, E. F., STANA GENE; CHARK, E. F., STAN	18p2 985 1010 0.00951 -0.10 0.70 SPI PIST CICLAIN's NULL; 18p2 319 375 0.00017 -0.77 0.27 SPI PIST CICLAIN's NULL; 18p2 985 1010 1.9e-05 -0.54 0.99 SPI PIST CICLAIN's NULL; 18p2 985 1010 1.9e-05 -0.11 0.05 CICLAIN's NULL; 18p3 0.15 0.22 CICLAIN'S SI RNA GENE; CICLAIN'S SI RNA GENE; 18p3 0.15 0.22 CICLAIN'S ANA CENE; 18p3 0.22 CICLAIN'S ANA CENE; 18p3 0.22 CICLAIN'S ANA CENE; 18p3 0.22 CICLAIN'S ANA CENE	1451 985 1010 0.00051 -0.10 0.70 SP.1P3-CHAIN-NULL; 75 147 0.27 0.27 SP-1P3-CHAIN-NULL; 75 147 0.27 0.27 CHAIN-N-1-S-S-NA-GENE; 75 0.27 CHAIN-N-1-S-NA-GENE; 75 0.27 0.27 0.27 0.27 0	14p1 985 1010 0.00051 -0.10 0.70 SPI IST CHAIN: NULL; 15p2 349 375 0.00017 -0.17 0.27 SPI IST CHAIN: NULL; 15p2 985 1010 15p-03 -0.54 0.50 SPI IST CHAIN: NULL; 11p3 A 377 468 6.8e-17 -0.11 0.05 TRANSCRIPTION FACTOR IIIN; CHAIN: E, F; CHAIN: E, F; CHAIN:	1872 349 375 0.000371 -0.10 0.70 SPIPS; CHAIN: NULL; 1872 349 375 0.00017 -0.77 0.27 SPIPS; CHAIN: NULL; 1872 1010 1.9e-05 -0.54 0.90 SPIPS; CHAIN: NULL; 1873 1877 468 6.8e-17 -0.11 0.05 CHAIN: A; SRINA CENE; CHAIN: E, F; CHAIN: E, F	Hep 985 1010 0.00051 -0.10 0.70 SPIPS; CHAIN: NULL; 75 1 1 1 1 1 2 2 349 375 0.00017 -0.77 0.27 SPIPS; CHAIN: NULL; 75 1 1 2 2 3 3 3 3 3 4 4 4 5 4 4 4 4 4 4	18p2 985 1010 0.00051 -0.10 0.70 SP. 195; CHAIN: NULL; 75 18p2 375 0.00017 -0.77 0.27 SP. 195; CHAIN: NULL; 75 18p2 385 1010 1.9-05 -0.34 0.90 SP. 195; CHAIN: NULL; 75 18p2 386 38-17 -0.11 0.05 CHAIN: NULL; 75 18p2 386 38-17 -0.11 0.05 CHAIN: E. P. RAA GENE; 75 18p2 CHAIN: E. P. CHAIN: E. P	1872 349 375 0.000371 -0.10 0.70 SPIPS; CHAIN: NULL; 1872 1910 0.000371 -0.11 0.27 0.27 SPIPS; CHAIN: NULL; 1873 1910 1.98-05 -0.454 0.90 SPIPS; CHAIN: NULL; 1911 1922 1910 1.98-05 -0.454 0.90 SPIPS; CHAIN: NULL; 1911 1923 1912 1913 1912 1913	Hep 985 1010 0.00051 -0.10 0.70 SPIPS; CHAIN: NULL; 75 1 1 1 1 1 2 2 3 3 5 0.00017 -0.77 0.27 SPIPS; CHAIN: NULL; 75 1 1 2 2 3 3 3 3 4 3 4 4 5 4 4 5 4 4 5 4 4	14p1 985 1010 0.00051 -0.10 0.70 SP.1P3-CHAIN-NULL; D. 15p2 339 375 0.00017 -0.77 0.27 SP-1P2-CHAIN-NULL; D. 15p2 1010 1.9-05 -0.34 0.90 SP-1P2-CHAIN-NULL; D. 15p3 1010 1.9-05 -0.34 0.90 SP-1P2-CHAIN-NULL; D. 15p3 1010 1.9-05 -0.34 0.90 SP-1P2-CHAIN-NULL; D. 15p3 1010 1.9-05 0.34-18 0.11 0.05 CHAIN-NULL; D. 15p3 CHAIN-NULL; D. 15p3 1010 1.9-05 0.34-18 0.15 0.23 CHAIN-S. P. P. CHAIN-S. P. P. CHAIN-S. P. P. CHAIN-S. P. P. CHAIN-S. P. P. CHAIN-S. P. P. CHAIN-S. P. P. CHAIN-S. P. P. CHAIN-S. P. P. CHAIN-S. P. P. CHAIN-S. P. P. CHAIN-S. P. P. CHAIN-S. P. P. CHAIN-S. P. P. CHAIN-S. P. P. CHAIN-S. P. P. CHAIN-S. P. P. P. CHAIN-S. P.	1872 349 375 0.000351 -0.10 0.70 SPIPS; CHAIN: NULL; 72 1872 349 375 0.00017 -0.77 0.27 SPIPS; CHAIN: NULL; 73 1872 349 375 0.00017 -0.17 0.27 SPIPS; CHAIN: NULL; 74 1872 377 468 6.8e-17 -0.11 0.05 TRANSGEPTON FACTOR HIM; CHAIN: E, F; CHAIN

PDB annotation	COMPLEX (TRANSCRIPTION) REGULATION/DNA) TEILIA, 5S GENE, NAR, TEILIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION) KEGULLATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DIA), COMPLEX (TRANSCRIPTION REGULATION/DIA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGILA TONOWDAY) YNG-YANG 1; TRANSCRIPTION, INITIATION, INITIATOR ELEMENT, YY1, ZINC2 FINGER PROTEIN, DIA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCREPTION)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2
Coumpound	TRANSORIPTON FACTOR IIIA; CHAIN: A, 58 RNA GENE; CHAIN: E, F;	TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA, CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	YYI; CHAIN: C; ADENO- SSCOCATED YRUS PS INITATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A. B.
SEQFOL D score					
PMF	0.64	0.47	0:00	0.29	0.28
Verify score	-0.17	-0.42	-0.65	-0.56	-0.39
Psi Blast	I.5e-2I	8.5e-34	1.76-28	7.6e-17	8.5e-31
END	0101	265	593	496	468
STAR T AA	929	405	472	351	354
CHAI N ID	V	¥	∢	O	o
PDB	£	1116	Itf6	Jubd	lubd
SEQ UD NO:	1015	1015	1015	1015	1015

PDB annotation	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRPTION REGULATIONDNA) YING-YANG I; TRANSCRPTION INITIATION, INITIATOR ELEMENT, YYI, ZINC 2 FINGER PROTEIN, DIAA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCRPTION REGULATIONDNA) TING-YANG I; TRANSCRPTION INITIATION, INITIATOR ELEMENT, YYI, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRPTION)	COMPLEX (RANSCRPTION REGULATION/DNA) TING-Y-ANG I; TRANSCRETION INITIATION, INITIATOR ELEMENT, YYI, ZINC 2 PRIGRE PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRETION)	COMPLEX (TRANSCRIPTION REGULATION/DIA), YING-YANG I; TRANSCRIPTION INITIATION, INITIATION ELEMENT, YYI, ZINC 2 FINGER PROTEIN, DIA-PROTEIN REGOGNITION, 3 COMPLEX
Coumpound		YYI; CHAIN: C, ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHANN: C; ADENO- ASSOCIATED VIKUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C, ADBNO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DIA; CHAIN: A, B;	YYI, CHAÏN: C, ADENO. ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAÎN: A, B;
SEQFOL D score					
PMF		0.47	0.54	0.57	-0.18
Verify		-0.13	-0.38	-0.26	0.04
Psi Blast		1.7e-31	5.1e-30	le-31	6.8e-28
END		497	527	584	953
STAR T AA		384	412	479	813
CHAI		o	U	S	၁
FDB TD		lubd	lubd	Jubd	1ubd
SEQ No B		1015	1015	1015	1015

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PDB annotation	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION	INITIATOR ELEMENT, YY1, ZINC2	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION PEGIT ATTOMONA)	TRANSCRIPTION REGIT ATTOM	TOTAL MICHIGAN MICHIGAN	ADRI ZINC FINGER NAME	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION,	ADRI, ZINC FINGER, NMR	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION,
Coumpound		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA:	CHAIN: A, B;			YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	CHAIN: A, B;				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;				ADR 1: CHAIN: NITH I :	treat, or man, room,		ADR1; CHAIN: NULL;			ADR1; CHAIN: NULL;	
SEQFOL D score																										
PMF		0.00				0.84						0.81							0.19			0.39			0.09	
Verify		0.13				0.22						-0.56							-0 66	2		-0.80			0.39	
Psi Blast		3.4c-30				3.4e-34						5.1e-27							6.8e-12.			8.5e-15			3.4e-16	
END		186				9001						1086							403			558			955	
STAR T AA		848				806						933							349			503			106	_
CHAI N ID		Ü				၁						S														
PDB ID		pqnI				Inbd						Inbd							2adr			2adr			2adr	
seQ No: D		1015				1015						1015							1015			1015			1015	

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PDB annotation	ADR1, ZINC FINGER, NMR	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR			COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;
Coumpound		ADRI; CHAIN: NULL;	COMPLEX(TRANSCRIPTION REGULATIONIDNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMITRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH ZDRP 3 DNA ZDRP 4	ZINČ FINGER PROTEIN GLJ1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D score									
PMF		0.80	0.11	0.01	0.21	0.10	0.71	0.28	0.15
Verify		-0,01	-0.30	-0.47	-0.36	-0.44	-0.34	-0.29	-0.67
Psi Blast		6.8e-18	3.4e-06	8.5e-10	3.4e-18	1.5e-26	6.8e-33	8.5e-33	5.1e-28
END AA		1015	428	556	428	467	556	583	593
STAR T AA		957	372	501	354	358	404	451	479
CHAI N ID			∢	₹	Ą	¥	¥	¥	A
PDB		2adr	2drp	2drp	2gli	2gli	2gii	2gli	2gli
SEQ NO:		1015	1015	1015	1015	1015	1015	1015	1015

				_		 		_		
PDB annotation	GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)			OXIDOREDUCTASE PERROCYTOCHROME CLOXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE; CYTOCHROME(C)-OXYGEN, CYTOCHROME C2 OXIDASE	PEPTIDE SYNTHETASE GRSA; PEPTIDE SYNTHETASE, GRSA, ADENYLATE FORMING	OXIDOREDUCTASE OXIDOREDUCTASE, MONOOXYGENASE, PHOTOPROTEIN, LUMINESCENCE		COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGERIDNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2
Coumpound		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER DNA BINDING DOMAIN ZINC-FINGER (ZFY- SWAP) (NMR, 12 STRUCTURES) 7ZNF 3		CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q,	GRAMICIDIN SYNTHETASE 1; CHAIN: A, B; PHENYLALANINB; CHAIN: C, D;	LUCIFBRASE; CHAIN: NULL;		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C:	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
SEQFOL D score						139.53	133,28		76.54	97.35
PMF		96'0	0.31		-0.17					
Verify score		-0.18	-0.23		10:0					
Psi Blast		1e-33	3.4e-05		3.4e-88	0	0		3.4e-29	1.7e-50
END AA		1010	1013		299	610	809		184	239
STAR T AA		106	586		1	48	59		86	157
CHAI N ID		٧ `			V	<			V	U
PDB CI		2gli	7znf		20cc	lamu	Ilei		lath	Imey
SEQ NO IB		1015	1015		1021	1023	1023		1028	1028

PDB annotation	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATIONDNA) COMPLEX (TRANSCRIPTION REGULATIONDNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION BEGULATIONNON) YING-YANG I; TRANSCRIPTION, INITATION, INITATION ELBERNY, YYI, ZINC2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION) NOMPLEX REGULATION/DNA)	COMPLEX (DNA-BINDING PROTEINDNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION		COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE,
Coumpound		TFIIIA; CHAIN: A, D; 58 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	YYY: CIAIN: C; ADBNO- ASSOCIATED VIRUS PS INITATOR ELEMENT DIA; CIAIN: A, B;	ZINC FINGER PROTEIN GLJI; CHAIN: A; DNA; CHAIN: C, D;	HEMOLIN; CHAIN: A, B;	CATALYTIC ANTIBODY 17E8 COMPLEXED WITH PHENYL [1-(1-N-(1-N-1)) CCCNYLAMINOPENTYL] (EAP 3 PHOSPHONATE 1EAP 4	INTERLEUKIN-I BETA; CHAIN: A; TYPE I INTERLEUKIN-I RECEPTOR; CHAIN: B;
SEQFOL D score		106.38	87,68	87.54	65.92	55.72	51.71
PMF							
Verify							
Psi Blast		1.4e-36	6.8e-35	3.4e-31	6.8e-48	1.7e-10	1.7e-34
END AA		269	239	240	351	348	353
STAR T AA		26	130	66	_	133	54
CHAI N ID		∢	v	. ¥	٧	В	В
PDB ID		1476	lubd	2gli	169	Icap	di l
SEQ ID NO:		1028	1028	1028	1029	1029	1029

PDB annotation	GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)	COMPLEX [IMMUNGOLOBULIN/RECEPTOR) [IMMUNGOLOBULIN/RECEPTOR) [ICR VAPUHA VBETA DOMANI; T- CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLON/OFTPIC, 2 [IMMUNGCIAPUR)		TRANSFERASE FPS; TRANSFERASE, ISOPRENE BIOSYNTHESIS, CHOLESTEROL BIOSYNTHESIS	TRANSFERASE FPS; TRANSFERASE, ISOPRENE BIOSYNTHESIS, CHOLESTEROL BIOSYNTHESIS				COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (RUHBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDRO1ASE 2 MOLECULAR RECONITION, BEPTOPE MAPPING, LEUCINE-RICH 3 REPRATS	COMPLEX (NUCLEAR
Coumpound		KBS-C20 T-CELL ANTIGEN RECEPTOR; CRAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	IMMUNOGLOBULIN ANTIGEN- BINDING FRAGMENT (FAB) (IGG2B, KAPPA) IMAM 3	FARNESYL DIPHOSPHATE SYNTHASE; CHAIN: NULL;	FARNESYL DIPHOSPHATE SYNTHASE; CHAIN: NULL;	DEFENSIN DEFENSIN /HNP\$-3 IDFN 3	DEFENSIN DEFENSIN /HNP\$-3 1DFN 3	DEFENSIN DEFENSIN /HNP\$-3 IDFN 3	RIBONUCLEASE INHIBITOR; CHAIN: A, D, ANGIOGENIN; CHAIN: B, E;	U2 RNA HAIRPIN IV; CHAIN: Q,
SEQFOL D score		59.81	56.22		70.74	58.55				
PMF score				0.11			00.1	00.1	0.35	0.78
Verify score				-0.31			-0.35	-0.35	-0.15	0.44
Psi Blast		1.7e-08	1.2e-11	5.1e-66	5.1e-66	1.1e-12	1.le-12	5.10-11	5.7e-22	3.8e-24
END		351	349	398	397	191	191	191	224	208
STAR T AA		133	139	57	65	132	133	133	99	89
CHAI N ID		#	=			4	¥	A	4	4
PDB ID		1kb5	Ima m	luby	luby	ldfin	1dfh	Idfin	la4y	1a9n
SEQ ID NO:		1029	6701	1031	1031	1032	1032	1032	1034	1034

РDВ annotation	PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	CELL ADHESION NEURAL CELL ADHESION	GROWTH FACTOR/GROWTH PACTOR REAZENOR FORR, IMMUNOLIOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR(GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH ACTOR RESEPTOR FORF, FGRR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL
Coumpound	R; UZ A; CHAIN: A, C; UZ B"; CHAIN: B, D;			U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	AXONIN-1; CHAIN: A;	FIBROBLAST GROWTH FACTOR S. CHAIN. S, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR S; CHAIN; S; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN; C, D;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;
SEQFOL D score									
PMF		0.57	0.80	0.62	0.05	0.22	0.25	0.74	0.58
Verify		0.15	0.52	0.21	0.12	0.27	0.15	0.22	0.13
Psi Blast		1.3e-21	1.1e-23	9.5e-21	3.8e-06	7.6e-07	1.5e-06	8.5e-19	1.9e-24
END		249	208	249	363	364	367	981	223
STAR T AA		83	88	33	279	. 283	283	39	4
CHAI N ID		٧	S	υ υ	A	υ	Д	٧	4
FDB U		la9n	la9n	la9n	lcs6	lcvs	levs	1006	1d0b
SEQ NO:		1034	1034	1034	1034	1034	1034	1034	1034

PDB annotation	ADHESION	TRANSFERASE CRYSTAL	STRUCTURE, RAB	GERANYLGERANYLTRANSFERASE,	2.0 A 2 RESOLUTION, N-	FORMYLMETHIONINE, ALPHA	SUBUNIT, BETA SUBUNIT	THE ANICORD A CONTROLLAY	STRINGTER DAD		2 0 A 2 RESOLUTION N.	FORMYI METHIONINE AI PHA	SUBINIT BETA SUBINIT		CONTRACTILE PROTEIN LEUCINE-	RICH REPEAT, BETA-BETA-ALPHA	CYLINDER, DYNEIN, 2	CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE-	RICH REPEAT, BETA-BETA-ALPHA	CYLINDER, DYNEIN, 2	CHLAMYDOMONAS, FLAGELLA	_	_	GL COPROISIN	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF2; FGFR2;	IMMUNOGLOBULIN (IG)LIKE	DOMAINS BELONGING TO THE I-	SET 2 SUBGROUP WITHIN IG-LIKE	DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2;
Coumpound		RAB	GERANYLGERANYLTRANSFE	RASE ALPHA SUBUNIT;	CHAIN: A, C; RAB	GERANYLGERANYLTRANSFE	RASE BETA SUBUNIT; CHAIN:	2,2	GER ANYL GER ANYL TR ANSEE	BASE AT PHA STRINITE	CHAIN: A C. RAB	GER ANYI GER ANYI TR ANSER	RASE BETA SUBUNITY CHAIN:	B, D;	OUTER ARM DYNEIN; CHAIN:	Α;			OUTER ARM DYNEIN; CHAIN:	A;			NEURAL CELL ADHESION	MOLECULE; CHAIN: A, B, C, D;	THE CASE AND ASSESSED.	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B, C, D;	FIBROBLASI GROWTH	FACTOR RECEPTOR 2; CHAIN:	E, F, G, H;		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D;
SEQFOL D score																																
PMF		0.03						100	-0.01						0.10				0.04				0.98		44.0	0.33						0.77
Verify score		-0.25						0.05	0.0						-0.76				-0.56				0.10		31.0	CI.0						0.12
Psi Blast		Ie-09						100.10	07-26-10						1e-08				7.6e-21				5.7e-07		16.00	1.36-05					000	3.8e-06
END AA		218						300	662						245				208				358		040	3/3					0.50	358
STAR T AA		106						90	ę.						104				45				279		240	0/7						583
CHAI N ID		A						-	<						V				Ą				Ą		p	4						5
PDB		1dce						Topo	2001						6sp1				lds9				lepf		Carl	Tev2					5	Tev2
SEQ NO:		1034						1024	ŧ01						1034				1034				1034		1034	FC0I					1001	1034

PDB annotation	IMMUNOGLOBULIN (FG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	RNA BINDING PROTEIN TAP (NEXI); RIBONUCLEOPROTEIN (RNP RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	RNA BINDING PROTEIN TAP (NFXI); RIBONUCLEOPROTEIN (RNP, RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	IMMUNOGLOBÜLIN-LIKE DÖMAIN CONNECTIN 127, TITIN 1G REPEAT 27; MUSCLE PROTEIN, IMMUNOGLOBULIN-LIKE DOMAIN		NERVE GROWTH PACTOR/TRKA COMPLEX, TRKA RECEPTOR, NERVE GROWTH FACTOR, CYSTEINE KNOT, 2 IMMUNOCLOBULIN LIKE DOMAIN, NERVE GROWTH FACTOR/TRKA COMPLEX	TRANSCRIPTION RNA IP; RANGAP; GTPARE-ACTIVATING PROTBIN FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNA IP, RANGAP, LTRA, LESCOME 2 RICH REPEAT PROTEIN, TWINNING.
Coumpound	FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	TITIN, 127; CHAIN: NULL;	MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) ITINM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 1TNM 58	NERVE GROWTH FACTOR; CHAIN: Y, W; TRKA RECEPTOR; CHAIN: X, Y;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;
SEQFOL D score							
PMF		0.25	0.05	0.01	0.34	-0.19	0.24
Verify		-0.40	-0.61	0.21	0.23	0.25	-0.34
Psi Blast		0.0013	0.00076	5.7e-06	1.7e-06	1.7e-09	7.6e-19
END		230	236	356	358	490	861
STAR		183	183	280	279	394	44
CHAI N ID		<	Д			×	∢
PDB		1fo1	1fo1	朝	Trum Trum	Iww w .	Iyrg
SEQ NO:		1034	1034	1034	1034	1034	1034

		,		_				 	
PDB annotation	HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN- BINDING, GPI-ANCHOR, 2 NEURAL	ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN		TRANSFERASE CK, MSSA; NUCLEOTIDE MONOPHOSPHATE KINASE,, TRANSFERASE	TRANSFERASE TRANSFERASE	TRANSFERASE APS KINASE; APS KINASE, ADENYLYLSULFATE KINASE, SULFATE, NUCLEOTIDE 2 KINASE, TRANSFERASE	COMPLEX (GIYDROLASE/COFACTOR) TRIACYLGIYCEROL LIPASE; COMPLEX (HYDROLASE/COFACTOR), LIPID	DEORANDATION SERINE ESTERAGE RELATED PROTEIN 2 LIPASE; SERINE ESTERAGE, HYDROLASE, LIPID DEGRADATION, PANCEAS, 2 GLYCOPROTEIN, CHIMERIC
Coumpound		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;			CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	GLYCEROL-3-PHOSPHATB CYTIDYLYLTRANSFERASE; CHAIN: A, B;	ADENOSINE- SPHOSPHOSULFATE KINASE; CHAIN: A, B;	TRIACYLGLYGEROL ACYL- HYDROLASB; CHAIN: A, C; COLIPASE; CHAIN: B, D	RP2 LIPASB; CHAIN: NÜLL;
SEQFOL D score								112.24	107.65
PMF		0.46			0.12	0.18	0.35		
Verify		0.40			-0.10	0.18	-0.55		
Psi Blast		9.5e-07			0.0019	1.1e-11	1.9e-05	0	0
END		358			519	312	393	319	316
STAR		279			360	193	359	-	5
CHAI		∢			∢	∢	¥.	∢	
10B		Эпст			1cke	Icoz	146j	leth	1gpl
SEQ ID NO:		1034			1035	1035	1035	1038	1038

PDB annotation			HYDROLASE HYDROLASE, LIPID DEGRADATION, PANCREATIC LIPASE		COMPLEX (DNA-BINDING PROTEINDINA) GHF-1; COMPLEX PONA-BINDING PROTEINDINA), PITUTARY, CPHD, 2 POU DOMAIN, TRANSCRIFTION FACTOR	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN,
Coumpound	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) (TRIACYLGLYCEROL HYDROLASE) 1HPL 3	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED ILPB 3 BY UNDECANE PROSPHONATE METHYL BSTER (TWO	PANCREATIC LIPASE RELATED PROTEIN 1; CHAIN: NULL;	DNA-BINDINO PROTEIN ANTENAM-EDIA PROTEIN (HOMEODOMAIN) MUTANT WHT CYS 39 HALD 3 REPLACED BY SER (CSS) COMPLEX WITH DNA (NMR, 1 AND 4 16 STRUCTURES) IAHD 1	PIT-I; CHAIN: A, B; DNA; CHAIN: C, D;	HOMEOBOX PROTEIN HOX-BI; CHAIN: A; PBXI; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN
SEQFOL D score	107.77	109.40	100.01				
PMF				1.00	0.65	1.00	1.00
Verify				0.19	-0.39	0.20	0.33
Psi Blast	0	0	0	3.4e-34	3.8e-26	1.7e-27	5.1e-29
END	318	316	316	219	213	215	212
STAR T AA	-	_	2	154	145	158	158
CHAI	¥.	В		e.	∢	۷.	v
EDB CI	Ihp	11pb	<u>l</u> ė	lahd	Iau7	1b72	158i
SEQ TO	1038	1038	1038	1044	1044	1044	1044

PDB annotation	HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY	COMPLEX (DNA-BINDING PROTEIN/DNA, DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA, DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	DNA BINDING PROTEIN 1TF-1 HD; 1FT1 8 DNA BINDING PROTEIN, HOMEODOMAIN, TRANSCRIPTION FACTOR 1FTT 19		COMPLEX (HONEODOMATIVONA) VINDINK, 2 HOMEODOMATIN VENTRAL NERVOUS SYSTEM HOMEODOMATIN, HOMEOBOX, DNA-BINDING PROTEIN, EMBRYOUG 2 DEVICED PMERY; COMPLEX (HOMEODOMATIN)DOMATIN	COMPLEX (HOMEODOMAIN/DNA) VIDDINAC HOMEODOMAIN, VERTRAL NIRKVOUS SYSTEM HOMEODOMAIN, HOMEOBOX, DIVA-BINDING PROTEIN, EMBRY ONLO, DEVELOPMENT, COMPLEX (HOMEODOMAIN/DNA)	Vienes,
Coumpound	EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	THYROID TRANSCRIPTION FACTOR I HOMEODOMAIN; IFTT 6 CHAIN: NULL; IFTT 7	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) 1FTZ 3	HOMBOBOX PROTEIN VND, CHAIN: P; DNA; CHAIN: A, B;	HOMEOBOX PROTEIN VND; CHAIN: P, DNA, CHAIN: A, B,	DNA-BINDING PROTEIN
SEQFOL D score						50.85		
PMF		1.00	1.00	96.0	66'0		1.00	66.0
Verify		0.16	0.09	0.03	0.16		0.26	0.30
Psi Blast		7.6e-26	1.9e-23	1.9e-23	5.1c-29	6.8e-20	1.9e-25	8.5e-32
END		213	211	216	212	223	215	219
STAR T AA		153	155	155	153	146	153	160
CHAI N ID		V	В			d.	۵,	
PDB		101	101	₫	Ifiz	Ink2	lnk3	Isan
SEQ No:		1044	1044	1044	1044	1044	1044	1044

PDB annotation	EEN CANT CANT D D DARR, 20	TTOR; COMPLEX (IMBITORANUCLEASE) COMPLEX (CHAINCIANCEASE), COMPLEX (RAINCIANCEASE), MOLECULAR RECOGNITION, BETTORE MARPING, LEUCING-RICH 3 REPEATS	PHATE TRANSPERASE CK, MSSA; NUCLEOTIDE MONOPHOSPHATE KINASE: TRANSFERASE		E/CY		1
Coumpound	ANTENNAPEDIA PROTEIN (HOMEDODANAIN) MUTANT WITH CYS 39 ISAN REPLACED BY SER AND RESIDUES I-6 DELETED (C3S, DEL I-6) ISAN 4 (NMK, 20 STRUCTURES) ISAN 5	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	ADENOSINE- SPHOSPHOSULFATE KINASE; CHAIN: A, B;	URIDYLMONOPHOSPHATE/CY TIDYLMONOPHOSPHATE KINASE; CHAIN: A;	SHIKIMATE KINASE; CHAIN: A, B;	TRANSFERASE URIDYLATE
SEQFOL D score							
PMF		0.46	0.40	0.33	0.99	0.84	9.64
Verify score		0.27	-0.08	0.08	0.34	-0.06	0.35
Psi Blast		0.0095	6.8e-22	3.4e-23	1.7e-21	1.7e-20	1.4e-19
END		214	187	187	185	186	185
STAR T AA		14	9	n	e .	→	9
CHAI		٧	V	٧	<	₹.	
EDG TD		la4y	1cke	146	Opl	1shk	Iukz
SEQ No.		1046	1048	1048	1048	1048	1048

				_		-		_			_	_	_			_			_	-		
PDB annotation		TRANSFERASE CK; NUCLEOTIDE MONOPHOSPHATE KINASE, TRANSFERASE			COMPLEX (HORMONE/RECEPTOR) HGH; HGHBP; COMPLEX	(HORMIONE/RECEPTOR)	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	RECEPTOR RECEPTOR, SIGNAL	TRANSDUCER OF IL-6 TYPE	CYTOKINES, THIRD 2 N-TERMINAL	DOMAIN, TRANSMEMBRANE,	RECEPTOR RECEPTOR, SIGNAL	TRANSDUCER OF IL-6 TYPE	CYTOKINES, THIRD 2 N-TERMINAL	DOMAIN, TRANSMEMBRANE,	RECEPTOR RECEPTOR, SIGNAL	TRANSDUCER OF IL-6 TYPE	CYTOKINES, THIRD 2 N-TERMINAL	DOMAIN, TRANSMEMBRANE,	DETCOPROTEIN	TRANSDUCER OF IL-6 TYPE	CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE,
Coumpound	COMPLEXED WITH ADP AND AMP 1UKZ 3	CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	TRANSFERASE(PHOSPHOTRA NSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4		GROWTH HORMONE; CHAIN: A; GROWTH HORMONE	RECEPTOR; CHAIN: B;	HEMOLIN; CHAIN: A, B;	GP130; CHAIN: NULL;				GP130; CHAIN: NULL;				GP130; CHAIN: NULL;				OBIGO CHANGARIA	OF 130, CHAIN: NOLL;	
SEQFOL D score																						
PMF		0.12	0.22		0.48		-0.14	0.42				0.33				0.01				0.35	ć.	
Verify score		0.01	-0.02		0.18		0.21	0.35				0.07				0.27				0.05	3.0	
Psi Blast		1.7e-21	8.5e-22		1.7e-10		6.86-21	1.9e-14				3.8e-09				8.5e-12				5 7a 10	21-21-2	
AA END		187	184		349		338	350				461				568				47.4	ř	
STAR T AA		9	· ·		162		74	253				360				477				5772	3	
CHAI N ID		¥			В		∢															
EDB CII		2cmk	3adk		laxi		ug.	16j8				1bj8				1bj8				11:8	of or	
SEQ No.		1048	1048		1049	1	1049	1049				1049				1049				1040	}	

PDB annotation	GLYCOPROTEIN	HORMONE, RECEPTOR,	HOKMONE/GROW IN PACTOR	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	CONNECTIN 471, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	CONNECTIN 471, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	CONNECTIN 471, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6.2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6.2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6.2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
Coumpound		GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR;	CHAIN: B;	TITIN; CHAIN: NULL;	TITIN; CHAIN; NULL;	TITIN; CHAIN: NULL;	TITIN; CHAIN; NULL;	TITIN; CHAIN; NULL;	GP130; CHAIN: A, B;	GP130; CHAIN: A, B;	GP130; CHAIN: A, B;
SEQFOL D score											
PMF		0.05		0.77	0:30	0.25	0.15	0.55	-0.09	0.21	0.03
Verify		0.14		0.12	0.59	-0.02	0.09	0.28	0.02	-0.07	0.25
Psi Blast		1.2e-21		3.8e-15	3.8e-12	5.le-11	9.5e-14	3.8e-17	8.5e-19	1.9e-20	3.8e-12
END		354		259	351	572	578	675	363	347	479
STAR T AA		158		159	257	479	479	577	158	159	256
CHAI N ID		В							∀	∢	∀
PDB		1bp3		Ibpv	lbpv	lbpv	Ibpv	Ibpv	Ibqu	1bqu	1bqu
SEQ TD NO:		1049		1049	1049	1049	1049	1049	1049	1049	1049

PDB PDB	CHAI	STAR T AA	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
∢		358	581	1.7c-14	-0.05	0.10		GP130; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 GRESPTOR BETA SUBUNIT, SIGNAL ING DE OFFERM
<		479	189	6.8e-23	0.04	0.09		GP130; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6.2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
∢		256	352	3.8e-13	0.36	0.35		CYTOKINB RECEPTOR COMMON BETA CHAIN; CHAIN: A:	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN
∢		359	457	7.6e-09	0.28	-0.12		CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A:	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN
en en		159	356	9.5e-27	0.17	0.24		GRANULOCYTE COLONY- STIMULATING FACTOR; CHAIN: A, C; G-CSF RECEPTOR; CHAIN: B, D:	CYTOKINE G-CSF-R; CLASSI CYTOKINE, HEMATOPOIETIC RECEPTOR, SIGNAL TRANSDUCTION
m		360	564	7.6e-16	0.14	90.0		GRANULOCYTE COLONY- STIMULATING FACTOR; CHAIN: A, C; G-CSF RECEPTOR; CHAIN: B, D;	CYTOKINE G-CSF-R; CLASSI CYTOKINE, HEMATOPOIETIC RECEPTOR, SIGNAL TRANSDUCTION
		156	350	1.1e-34	-0.07	0.55		MORIGAL ADDISSION MOLECULE DROSOPHILA NEUROGLIAN CONTRAINED FRAGMENT CONTRAINED TRAINED THE ICEB 3 TWO ANNEO PROXIMAL FIBRONECTIN TYPE II FIBRONEC	
		255	456	1.9e-23	0.20	06:0		NEURAL ADHESION	

PDB annotation				CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL ADHESION
Coumpound	MOLECULE DROSOPHILA MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTR YPTIC FRAGMENT CONTANINO THE ICPB 3 TWO AMINO PROXIMAL. FIBRONECTIN TYPE III FIBRONECTIN TYPE III FIBRONECTIN TYPE III FIBRONECTIN TYPE III	MOLECULE DROSOPHILA MOLECULE DROSOPHILA CONTAINING THE ICE'S 3 TWO AMINO PROZUMAL. FIBRONBCTIN TYPE II FIBRONBCTIN TYPE III	MOLECULE DROSOPHILA MOLECULE DROSOPHILA MOLECULE DROSOPHILA CONTAINING THE ICEB 3 TWO AMMO PROXIMAL. FIBRONBCTIN TYPE III FIBRONBCTIN TYPE III	AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;
SEQFOL D score							
PMF		0.42	90.00	-0.20	80.0-	-0.17	0.10
Verify score		0.17	0.35	0.00	0.15	0.12	-0.08
Psi Blast		3.8e-31	81-91	6.8e-23	1.7e-35	3.4e-15	6.8e-30
END		519	0.20	671	349	750	464
STAR T AA		475	479	272	2	350	1.9
CHAI N ID				¥.	¥	A	∢
PDB ID		1cfb	lofb	1cs6	1086	lcs6	lcs6
SEQ ID NO:		1049	1049	1049	1049	1049	1049

F SKDFOL Coumpound PDB manotation GRANULOCYTE COLONY- RICHALTHOR ACTOR STANLIATING ACTOR RECEPTOR, CHARK, NULL; GRANULOCYTE COLONY- STANLIATING TACTOR RECEPTOR, CHARK, NULL; GRANULOCYTE COLONY- STANLIATING TACTOR RECEPTOR, CHARK, NULL; FIREOBLAST GROWTH FACTOR RECEPTOR CHARK, NULL; CATOR RECEPTOR CHARK, NULL; FIREOBLAST GROWTH FACTOR ACTOR RECEPTOR CHARK, NULL; CATOR RECEPTOR CHARK, NULL; FIREOBLAST GROWTH FACTOR ACTOR RECEPTOR CHARK, NULL; FIREOBLAST GROWTH FACTOR RECEPTOR CHARK, NULL; FACTOR RECEPTOR CHARK, NULL; CATOR RECEPTOR CHARK, NULL; FACTOR RECEPTOR CHARK,
Deore Discord
PMF 8core 0.04 0.09 0.09 0.19 0.19
Verity score -0.16 -0.12 -0.47 -0.25 -0.01
Pal Blast 7.6e-13 3.8e-13 7.6e-10 6.8e-31 1.5e-15 1.7e-28
AA AA AA AAA AAA AAA AAA AAA AAA AAA A
259 259 274 74 74 74
N N D D D D D D D D D D D D D D D D D D
PDB Into Into Into Into Into Into Into Into
SECQ NO. 1049 1049 1049 1049

PDB annotation	EPTOR, EPOBP, ERYTHROPOIETIN, ERYTHROPOIETIN BRCEETOR, SIGNAL 2 TRANSDICTION, HEMATOPOIETIC CYTOKINE, CYTOKINE RECEPTOR 3 CLASS 1, COMPLEX (CYTOKINERECEPTOR)	á,	DN CELL ADHESION NCAM; NCAM, B, C, D; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN		GROWTH FACTOR/GROWTH C, D, PACTOR REGEPTOR RUZ; FGRQ; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I. SET? SEUGROUP WITHIN (LOLLIKE DOMAINS, B-TSEFOLL FOLL)	GROWTH FACTOR/GROWTH FACTOR REGEPTOR ROFE; FORPL; IMMUNOGLOBULIN (JG) LIKE DOMAINS BELONGING TO THE I. SETT SELBGROUP WITHIN CLIKE DOMAINS, B-TSEPOLL, FOLD.	
Coumpound	ER YTHROPOIETIN RECEPTOR; CHAIN: B, C;	NBURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	MOLECULE; CHAIN: A, B, C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH PACTOR I; CHANDIR A, B; FIBROBLAST GROWTH PACTOR RECEPTOR I; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH
SEQFOL D score							
PMIF		0.27	0.07	0.65	0.12	0.58	0.63
Verify score		0.02	0.13	-0.02	-0.14	-0.08	0.05
Psi Blast		3.8e-14	6.8e-13	1.7e-26	3.4e-30	5.7e-20	1.7e-26
END		222	234	250	254	213	250
STAR		29	Ľ	74	74	49	74
CHAI N ID		4	¥	ш	9	0	O
PDB TD		lepf	lepf	lev2	Iev2	lew	levt
SEQ NO.		1049	1049	1049	1049	1049	1049

PDB annotation	SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	HORMONICEGROWHTH ACTOR/HORMONE RECEPTOR 4 HELICAL BUNDLE, ALPHA HELICAL BUNDLE, RENARY COMPLEX, RN 2 III DOMAINS, BETA STREET DOMAINS, CTORKINE RECEPTOR COMPLEX RECEPTOR COMPLEX	HORMONE/GROWTH ACTOR/HORMONE RECEPTOR 4- HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TRENARY STREET PROMENS, FROM SET STREET DOMAINS, CYTOKINE- RECEPTOR COMPLEX	HORMONEGROWTH CHECKTOR 4- IREIGAL BUNDLE, ALPHA HELICAL BUNDLE, ALFHA COMPLEX, FR 2 III DOMAINS, BETA SEBET TOMAINS, CYTOKINE- REPETTOR COMPLEX RECEPTOR COMPLEX	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL		
Compound	C, D;	PLACENTAL LACTOGEN, CHAIN, A; PROLACTIN RECEPTOR; CHAIN: B, C; E; E; C;	PLACENTAL LACTOGEN, CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C; H H R	PLACENTAL LACTOGEN, CHAIN: A; PROLACTIN F RECEPTOR; CHAIN: B, C; H R R R R R R R R R R R R R R R R R R R	TELOKIN; CHAIN: A II	CELL ADHESION PROTEIN FIBRONECTIN CELL- ADHESION MODULE TYPE III- 10 1FNA 3	CELL ADHESION PROTEIN FIBRONECTIN CELL. ADHESION MODULE TYPE III- 10 IFNA 3
SEQFOL D score							
PMF		0.51	0.03	0.71	-0.20	0.16	-020
Verify		0.28	-0.23	-0.11	0.18	0.23	0.38
Psi Blast		3.4e-24	1.7e-16	7.6c-10	5.Ie-08	1.7e-13	6.8e-09
END		354	253	352	572	265	998
STAR T AA		160	70	192	475	486	779
CHAI N ID		В	m	o	4		
PDB ID		1f6f	1f6f	1f6f	Ifhg	Ifna	Ifna
SEQ D NO:		1049	1049	1049	1049	1049	1049

PDB annotation	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18	CELL ADHESION PROTEIN RGD, EXTRACEL LULAR MATRIX IFNF 18	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING	CELL ADHESION PROTEIN CELL	ADHESION PROTEIN, RGD, EXTRACELLILAR MATRIX 2	HEPARIN-BINDING,	CELL ADHESION PROTEIN CELL	EXTRACELLULAR MATRIX, 2	HEPARIN-BINDING, GLYCOPROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD,								
Coumpound	FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	FIBRONECTIN; IFNF 6 CHAIN: NULL; IFNF 7	FIBRONECTIN; 1FNF 6 CHAIN: NULL: 1FNF 7	FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	FIBRONECTIN; 1FNF 6 CHAIN: NULL: 1FNF 7	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: NULL;			FIBRONECTIN; CHAIN: NULL;			FIBRONECTIN; CHAIN: NULL;					
SEQFOL D score		166.16																
PMF	86.0		0.23	0.76	-0.20	0.55	0.07	-0.07	6I.0-	96.0	-0.20	1.00			1.00			0.49
Verify score	0.25		0.29	0.24	80.0	0.22	0.26	0.12	10.0	0.29	0.05	0.21			0.03			-0.04
Psi Blast	5.1e-36	5.10-36	3.4e-33	1.7e-26	3.4e-12	1.7e-20	3.4e-27	3.4e-23	8.5e-25	I.4e-18	3.4e-20	1.1e-27			3.4e-14			1.1e-20
END	595	575	998	459	716	564	664	751	855	333	716	343			343			456
STAR T AA	158	159	479	89	772	272	361	482	280	70	774	157			162			259
CHAI N ID						¥.	<	<	4	<	٧							
PDB DI	Ifnf	JųJI	Iff	ΙΨΈ	1finf	цфI	Ifih	lfih	Ifnh	Ifph	Ifnh	Imfi			lmfi			lmfn
SEQ UO:	6401	1049	1049	1049	1049	1049	1049	1049	1049	1049	1049	6401			1049			1049

PDB annotation	EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING,	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELULAR MATRIX, 2 HEARIN-BRODING, GY SCORD STATES	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GI YCOPROTFIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLUAR MATRIX, 2 HEPARIN-BINDING, GT YCOPROTEIN	MINSCLE PROTEIN CONNECTIN, INZTME, CELL ADHESION, GLYCOROTEIN, TRANSMEMBRANE, REBEAT, BRAIT, 2 IMMINOGLOBULIN FOLL, BRAIT SPLICING, SIGNAL, 3 MINSCLE PROTEIN	STRUCTURAL PROTEIN INTEGRIM, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
Coumpound		FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;	TITIN; CHAIN: NULL;	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;
SEQFOL D seore							
PMF		0.45	0.13	0.17	-0.05	1.00	0.99
Verify		0.13	0.05	0.24	0.20	0.16	0.19
Psi Blast		6.8e-11	3.4e-20	1.9e-27	6.8e-25	9.5e-23	1.2e-15
END		459	565	\$99	665	152	352
STAR T AA		272	360	482	482	5 9	160
CHAI N ID							V V
PDB ID		Imfn	a di	Imfi	fill	Inct	1923
SEQ NO:		1049	6401	1049	1049	1049	1049

PDB annotation	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN	STRUCTURAL PROTEIN INTEGRIN, HEMDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN	STRUCTURAL PROTEIN INTEGRIN, HEMDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN	STRUCTURAL PROTEIN INTEGRIN, HEMDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN	STRUCTURAL PROTEIN TENASCIN, I-BRONECTIN TYPE-III, HEPARIN, ESTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-II, HEPARIN, FARTACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-II, HEPARIN, ETRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN 127, TITIN 1G REPEAT 27, MUSCLE PROTEIN,
Coumpound	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	TITIN, 127; CHAIN: NULL;
SEQFOL D score		103.51						
PMF	0.59		0.43	99.0	0.43	-0.20	-0.20	0.15
Verify score	0.11		0.23	0.29	0.24	0.09	0.08	0.70
Psi Blast	3.4e-19	5.1e-26	5.1e-26	3.4e-17	6.8e-12	3.4e-08	3.4e-11	1.1e-19
END	569	677	663	248	564	862	971	150
STAR	361	479	481	8		711	776	9
CHAI	V	<	<	₹	∀	٧	¥.	
90 a	lqg3	1923	1983	Iqg3	1qr4	lqr4	1qr4	曹
SEQ No.	1049	1049	1049	1049	1049	1049	1049	1049

PDB annotation	IMMUNOGLOBULIN-LIKE DOMAIN			MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, I SET, MUSCLE PROTEIN	TRANSFERASE TRK RECEPTOR, RECEPTOR TYROSINE KINASE, 3D- DOMAIN SWAPPING, 2 TRANSPERASE	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOENESIS, PROTEIN 2 BINDING	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
Coumpound		MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN) ITMM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	GLYCOPROTEIN PIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 11TF 3	TWITCHIN 18TH IGSF MODULE; CHAIN: NULL;	NT-3 GROWTH FACTOR RECEPTOR TRKC; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: A;
SEQFOL D score										
PMF		0.84	-0.20	-0.09	0.59	10.0	99.0	0.16	0.10	0.04
Verify score		0.39	0.39	99:0	0.18	-0.00	0.55	0.76	0.02	-0.12
Psi Blast		1.9e-22	1.7e-09	1.9e-22	1.1e-21	9.5e-13	1.5e-14	9.5e-14	9.5e-10	1.9e-13
END		152	998	152	163	251	250	345	465	570
STAR T AA		<i>L9</i>	776	59	64	09	154	255	359	475
CHAI N ID					¥	¥	⋖	Α.	V.	٧
80 E		Itnm	Ήť	lwit	Iwwc	2fcb	2finb	2fnb	2ftrb	2fnb
SEQ No.		1049	1049	1049	1049	1049	1049	1049	1049	1049

	PDB annotation	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING			CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HERARIN- BINDING, GPL-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBELLIN POLD, HOMOPHILCS BINDING, CELL ADHESION PROTEIN	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	CELL ADHESION NEURAL CELL ADHESION	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION,
	Coumpound	FIBRONECTIN; CHAIN: A;	HORMONE/RECEPTOR HUMAN GROWTH HORMONE COMPLEXED WITH ITS RECEPTOR 31HR 3 SECEPTOR 31HR 4	HORMONERECEPTOR HUMAN GROWTH HORMONE COMPLEXED WITH ITS RECEPTOR 31HR 3 (EXTRACELLUIAR DOMAIN)	NETRAL CELL ADHESION MOLECULE, L'ARGE ISOFORN; CHAIN: A;	HEMOLIN; CHAIN: A, B;	AXONIN-1; CHAIN: A;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN:
	SEQFOL D score							
	PMF	0.28	0.13	0.03	0.46	-0.06	0.07	-0.05
tr.	Verify score	0.10	0.16	0.24	0.45	0.09	0.02	0.12
	Psi Blast	1.5e-16	le-10	3.8e-27	3.8e-23	3,4e-29	3,4e-34	3.4e-41
	END	019	349	351	154	157	158	157
	STAR T AA	574	162	162	59	20	4	es.
	CHAI N ID	*	m	æ	٧	4	A	S
	PDB UD	2fhb	3hhr .	3hhr	3пст	1bih	9821	levs
	Ş a Ş	1049	1049	1049	1049	1050	1050	1050

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PDB annotation	GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	TRANSDICTION 2 DIMERIZATION	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	CELL ADHESION NCAM; NCAM,	GLYCOPROTEIN GLYCOPROTEIN	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF2; FGFR2;	IMMUNOGLOBULIN (IG)LIKE	DOMAINS BELONGING TO THE I-	SET 2 SUBGROUP WITHIN IG-LIKE	DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF2; FGFR2;	IMMUNOGLOBULIN (IG)LIKE	DOMAINS BELONGING TO THE I-	SET 2 SUBGROUP WITHIN IG-LIKE	DOMAINS, B-1 KEFOIL FOLD	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF1; FGFR1;	IMMUNOGLOBULIN (IG) LIKE	DOMAINS BELONGING TO THE I-	SET 2 SUBGROUP WITHIN IG-LIKE	DOMAINS, B-TREFOIL FOLD	IMMUNE SYSTEM FC-EPSILON RI-	ALPHA; IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN, RECEPTOR, IGE-	BINDING 2 PROTEIN	IMMUNE SYSTEM, MEMBRANE
Coumpound	C, D;	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FACTOR RECEPTOR 1: CHAIN:	C, D;		NEURAL CELL ADHESION	MULECULE; CHAIN: A, B, C, D;	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B, C, D;	FIBROBLAST GROWTH	FACTOR RECEPTOR 2; CHAIN:	E, F, G, H;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B, C, D;	FIBROBLAST GROWTH	FACTOR RECEPTOR 2; CHAIN:	E, F, G, H;		FIBROBLAST GROWTH	FACTOR 1; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;		HIGH AFFINITY	IMMUNOGLOBULIN EPSILON	RECEPTOR CHAIN: A;		FC RECEPTOR
SEQFOL D score																															
PMF		0.33					0.64		0.05						-0.05						0.54						0.54				0.90
Verify		0.22					-0.00		80.0						0.21						80.0						0.19				-0.02
Psi Blast		6.8e-42					6.8e-22		1.7e-36						8.5e-14						le-41						1.7e-23				8.5e-24
END		157					143		157						162						157						162				159
STAR T AA		3					2		3						8			_			m						7				2
CHAI N ID		D					¥		13						ш						υ						¥				A
PDB ID		lcvs					lepf		lev2						lev2					1	levt						1129			_	
SEQ NO:		1050					1050		1050						1050					0000	1020						1050				1050 Ifcg

PDB annotation	PROTEIN CD32; PC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN- LIKE, RECEPTOR	MUSCLE PROTEIN CONNECTIN, NEXTMS; CELL ADHESION, GLYCOPROTEIN, THA ANSWERS AND	IRANGSMEMBRANG, MEFERI, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCIE, PROTEN	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN.	TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN		
Coumpound	FC(GAMMA)RIIA; CHAIN: A;	TELOKIN; CHAIN: A	TELOKIN; CHAIN: A	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	TITIN; CHAIN: NULL;		TITIN; CHAIN: NULL;		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 458	MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN) ITUM 3 (NMR. MINIMIZED
SEQFOL D score										
PMF		0.63	-0.14	0.31	0.87		-0.09		0.54	-0.12
Verify score		-0.10	0.37	0.00	0.07		0.20		0.43	0.07
Psi Blast		1.2e-12	3.4e-17	1.9e-20	1.2e-12		1.7e-16		1.2e-12	1.7e-16
END		75	157	147	7.5		158		75	158
STAR T AA		-	76	2	7		08		2	80
CHAI		V	A	¥						
FDB TD		1fbg	1fhg	1fbl	Inct		Inct		1thm	Itom
SEQ No:		1050	1050	1050	1050		1050		1050	1050

	_							
PDB annotation		IMMUNE SYSTEM PS8 NATURAL KILLER CELL RECEPTOR, KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTICEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	HISTOCOMPATIBILITY COMPLEX BR; BZM; PEPTIDE HLA BS, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	IMMUNOGLOBULIN FOLD	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK, CELL RECEPTOR, IMMUNOCLOBULIN 2 FOLD, RECEPTORAMHC COMPLEX,	
Coumpound	AVERAGE STRUCTURE) 1TNM 4 1TNM 58	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	PC GAMMA RIIB; CHAIN: A;	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HLA-A*0201; CHAIN: A, D; BETA-Z MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	HI.A-CW3 (HEAVY CHAIN); CHAIN: A; BETTA-2. CHAIN: B; MCROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORITIN ALPHA-2; CHAIN: C, NATURAL KILLER CELL RECEPTOR KILLERCAIN: D, E;	HISTOCOMPATIBILITY ANTIGEN MURINE CLASS 1
SEQFOL D score								
PMF		60.0	69.0	0.30	0.25	0.22	0.28	69.0
Verify		-0.26	0.14	-0.16	0.06	0.18	0.24	0.34
Psi Blast		1.9e-19	6.8e-25	3.40-43	3.4e-43	1.70-42	5.16-43	1.4e-42
END		146	160	115	115	115	115	116
STAR T AA		2	2	26	26	26	26	56
CHAI N ID		∢	∢	<	∢	∢	∢	<
PDB ID		2dli	2fcb	lain	lagd	Iduz	lefx	Ihoc
SEQ No. 19		1050	1050	1051	1051	1051	1051	1051

PDB annotation		,	COMPLEX MATCH RESPONSE AND	COMPLEX (MHC ÍPEPTIDE) VSV-8, MHC/PEPTIDE COMPLEX, TRANSMEMBRANE PROTEIN, THYMIC 2 SELECTION, COMPLEX (MHC !PEPTIDE)	COMPLEX (NR RECEPTORALIC CLASS I) H2 CLASS H4TOCOMPATIBILITY AND H4TOCOMPATIBILITY AND H4TOCOMPATIBILITY AND H4TOCOMPATIBILITY NRFACE BALLY CORROLLES IN RECEPTOR, MECT, C. TYPE LECTIFLARE, 3, MECT, C. TYPE LECTIFLARE, 3, MECT, C. TYPE LECTIFLARE, 3, MECT, C. TYPE LECTIFLARE, M. MACH, C. TYPE LECTIFLARE, A. MET, IVAS, METS/COMPATIBILITY BAN IVAS
Coumpound	MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING 1HOC 3 OF H-2D===, B2- MICROGLOBULIN, AND A 9- RESIDUE PEPTIDE 1HOC 4	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW8.1 ANTIGEN AW8.1 ANTIGEN IHSB 3 ANTIGEN) IHSB 4	HISTOCOMPATIBILITY HISTOCOMPATIBILITY ANTIGEN HIA-E, CHAIN: A, C, ETRA-S-AIGCROGOLÓBULN; CHAIN: B, PEPTIDE (WAAPKIVIL.); CHAIN: F, C;	MHC CLASS IH-2KB HEAVY CHAIN, CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; VESICULAR STOMATITIS VEULS NUCLEOPROTEIN; CHAIN: C.	MHC CLASS 1H-2DD HEAVY CHAN; CHMN-4, BETA-2 MICROGLOBULN; CHAIN; B; HEVELOED E GLYCOPROTEIN 120 PEPTIDS; CHAIN; P; LY49A; CHAIN; C, D; CHAIN; P; LY49A; CHAIN; C, D;
SEQFOL D score					
PMF		0.40	0.25	0.37	0.39
Verify		0.08	0.13	0.13	0.10
Psi Blast		8.56-44	8.5e-43	1.26-43	3.4e-42
END		115	115	115	115
STAR T AA		26	26	56	
CHAI N ID		∢	<	<	∢
PDB		Thsb	1mhe	losz	1903
SEQ NO ID		1051	1051	1051	1051

PDB annotation	LY-49		COMPLEX (ZINC FINGER/DINA) ZINC FINGER, PROTEIN-DIA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DINA)	COMPLEX (TRANSCRIPTION REGULATIONDNA) COMPLEX (TRANSCRIPTION REGULATIONDNA), RNA POLYMBRASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (DNA-BINDING PROTEINDNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	CALCIUM-BINDING PROTEIN CALB; CALCIUM-H-PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	
Coumpound		HISTOCOMPATIBILITY ANTIGEN TRUNCA (IED HUMAN CLASS II HUMAN CLASS II HUMAN COMPLEXED WITH ANTIGEN HLA-AWG ITMC 3 ANTIGEN HLA-AWG ITMC 3 DECAMERIC PEPTIM 5 EVAPPETHRK) ITMC 4	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2
SEQFOL D score			100.26	108.39	89.55	68.22	97.42
PMF		0.52					
Verify		0.43					
Psi Blast		8.5e-44	3.4e-49	8.5e-38	3.4e-34	5.10-37	3.4e-44
END		115	650	762	466	291	283
STAR T AA		26	268	969	327	160	154
CHAI N ID		٧	ပ	∢	٧	∢	
PDB ID		Itmo	Imey	1116	2gli	Ia25	Irsy
SEQ NO:		1051	1068	1068	1068	1070	1070

PDB annotation	73	GOMPLEX (GTP. AAAAA, TRAASDUCEN BETA I, TRAASDUCEN BETA SUBLIVIT; GAAAAAI, TRANSDUCIN GAAAAA SUSUMT, COMPLEX (GTP. BINDINGTRANSDUCEN, G PROTISH, HETROSTORIANER 2 SIGNAL TRANSDUCTING	CONDLEX (CIT) TH. BINDING/TRANSDICERS BETA!, BANSDICOR TRATS SIBMTH; GAMMAA!, TRANSDICOR TRATS SIBMTH; GAMMAA!, TRANSDICOR TRANSDICOR GAMAA BINDING/TRANSDICERS, G PROTEN, HETROTRANSDICERS, G PROTEN, HETROTRANSDICERS, G PROTEN, HETROTRANSDICERS, G PROTEN, HETROTRANSDICTION SIGNAL TRANSDICCTION	COMPLEX (ZINC FINGERDNA) ZINC GER FINGER, PROTEIN-DNA G: INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGERDNA)	E. COMPLEX (TRANSCREPTION REGULATION/RINA), COMPLEX (TRANSCREPTION REGULATION/RINA), RNA REGULATION/RINA, RNA TRANSCREPTION INITIATION, ZINC TRANSCREPTION INITIATION, ZINC	-
Coumpound	DOMAIN) (CALB) IRSY 3	GT-ALPHA/GI-ALPHA CHABERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	ZINC FINGER PROTEIN GLII;
SEQFOL D score		116.65	104,69	107.26	114.17	103.60
PMF						
Verify						
Psi Blast		5.1e-89	5.16-81	1.4e-48	16-37	1.4e-33
END		322	345	412	913	441
STAR T AA		-	m	330	750	302
CHAI N ID		д	Д	ပ	∢	Ą
20 CI		lgot	1got	Imey	1116	2gli
SEQ So di		1075	1078	1084	1084	1084

PDB annotation	GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	CONTRACTILE PROTEIN WHI DOMAIN; MOLECULAR RECOGNITION, ACTIN DYNAMICS, CONTRACTILE PROTEIN	CELL MOTHLITY AN INCOMPLETE SEVEN STRANDED ANTI-PARALLEL BET'S BARREL 2 CLOSED BY AN ALPHA HELLX EVIN DOMAIN, ACTIN-BASED CELL 3 MOTILITY, INTERACTION MODULE	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DIA) COMPLEX (TRANSCRIPTION REGULATION/DIA), RNA POLYMERASE II, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTIEN	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INTIATION, INTIATOR PIT PARENT VVI 770.7
Coumpound		MENA EVHI DOMAIN; CHAIN: A; PEPTIDE ACTA; CHAIN: B;	EVHI DOMAIN FROM BNAVASP-LIKE PROTEIN; CHAIN: A, B; PHE-GLU-PHE- PRO-PRO-PRO-THR-ASP- GLU-GLU; CHAIN: C, D;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLJGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, B; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A B:
SEQFOL D score		82.80	62.71	84.85		110.38	120.65	98.51
PMF								
Verify								
Psi Blast		3.4e-50	1.7c-44	1.7e-26		1.4e-45	3.4e-34	3.4e-33
END		122	121	473		200	530	444
STAR T AA		0	6	391		418	362	336
CHAI N ID		4	∢	A		υ	∢	2
PDB CI		levh	19c6	lalh		Imey	9311	Iubd
SEQ NO.		1090	1090	1095		1095	1095	1095

PDB annotation	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATIONDNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	CELL ADHESION PROTEIN	EPITHELIAL CADHERIN DOMAINS I AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION	CALCIUM-BINDING CALCIUM- BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR		
Coumpound		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	E-CADHERIN: CHAIN: A B-		N-CADHERIN; CHAIN: A;	TROPONIN C; CHAIN: NULL;	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	NEUROCALCIN DELTA; CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-DISENDENT PROTEIN YANG SP II CIDM 4	CALCIUM-BINDING PROTEIN
SEQFOL D score		105.76	122.19		122.52	73.76	92.24	184.52	57.84	67.88
PMF										
Verify										
Psi Blast		6.8e-34	5 10-48		6.88-50	8.5e-36	1.7e-39	1.7e-49	1.4c-55	3.4e-60
END AA		473	266		265	237	249	245	234	235
STAR T AA		334	62		19	72	74		83	82
CHAI N ID		4	4		٧		13	<	<	
EDB CI		2gli	1edh		Incj	laj4	Iaui	1bjf	lcdm	Icli
SEQ NO ID		1095	1011		1101	1105	1105	1105	1105	1105

PDB CHAI STAR END Phi Blast Vertry Part Store Commpound											_			_
PDB CHAI STAR END Pri Blast Vorlty PMF SEQPED	PDB annotation		CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCUIM-BINDING PROTEIN		CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION CALCIUM.	BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION	REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRACTION	CALCIUM-BINDING PROTEIN EF- HAND 1TNX 14		CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEN/OPETITIES)		COMPLEX (GTPASE- ACTIVATING/GTP-BINDING)	COMPLEX (GTPASE- ACTIVATING/GTP-BINDING), GTPASE ACTIVATION	TRANSPORT PROTEIN TC4; GTPASE,
PDB CHAI STAR END Pu Blast Verlty PMF	Coumpound	CALMODULIN (VERTEBRATE) ICLL 3	RECOVERIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN RECOVERIN (CALCIUM SENSOR IN VISION) IREC 3	TROPONIN C; CHAIN: NULL;			TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	BINDING PROTEIN SARCOPLASMIC CALCIUM- BINDING PROTEIN 2SCP 3	P50-RHOGAP; CHAIN: A, B, C; CDC42HS; CHAIN: D, E, F;		GTP-BINDING PROTEIN RAN;
PDB CHAI STAR END Pel Blast Verify	SEQFOL D score		160.57	143.82	73.38			96.69	73.36	68.28	53.97	70.86		74.78
PDB CIAAI STAR END Pal Biast	PMF													
PDB GIAA STAR EVD	Verify													
PDB CHAI STAR IN	Psi Blast		3.4e-39	1.7e-34	1.5e-39			1e-38	8.5e-40	3.4e-59	3.4c-09	6.80-48		8.5e-52
PDB CHAI DD N N DD N N DD N N	END		245	250	235			233	237	236	205	216		231
100 110	STAR		62	89	20			19	63	62	34	21		45
PDB DD DDB INC	CHAI									¥	A	Д		Ą
NO. NO. 11105 1105 11105 11105 11105 11105 11105 11105 11105 11105 11105 11105	PDB CD		liku	1rec	Itef			Itnx	Itop	lvrk	2scp	lam4		1byu
<u> </u>	gg e ö		1105	1105	1105			1105	1105	1105	1105	1114		1114

PDB annotation	NUCLEAR TRANSPORT, TRANSPORT PROTEIN	AN; TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN	KAP- SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS		SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINBTIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	-	TON PROTEIN TRANSPORT GDB.			, D; BEIA, P95 SMALL GIPASE, NUCLEAR TRANSPORT RECEPTOR	GTP-BINDING PROTEIN GTP-	BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS	GTP-BINDING GTP-BINDING,	GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY			GTPASE/NUCLEAR PROTEIN).
Coumpound	CHAIN: A, B;	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SEB DE CHAIR	KINASE CHAIN: B;	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN:	HIMAN ADP-RIBOSYI ATTON	FACTOR 1; 1HUR 5 CHAIN: A,	RAN; CHAIN: A, C; IMPORTIN	BETA SUBUNIT; CHAIN: B, D;	RAP2A; CHAIN: NULL;		RAC1; CHAIN: NULL;		RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN	NUP358; CHAIN: B, D;	
SEQFOL D score		69.65	67.97		75.99	82.44	71 40		86.05		79.99		77.42		89.47		
PMF																	
Verify score																	
Psi Blast		1.7e-52	1.7e-63		1.7e-62	1.5e-54	516-12		3.4e-51		3.4e-60		1.2e-54		3.4e-51		
END		231	216		217	222	218		221		217		222		231		
STAR T AA		41	20		20	47	37		52		20		49		47		_
CHAI N ID		В	A		¥	4	×		V						S		
10 GI		lbyu	lcly		lotq	lcxz	Ihm		1ibr		lkao		1mh1		Imp		
S e S		1114	1114		1114	1114	1114		1114		1114		1114		1114		

PDB annotation	TRANSPORT	COMPLEX(GTP ASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE),	GIPABEL TRANSITION STATE, GAP COMPLEK (GIP. BINDINGERECTOR), RAS-BEL/ATED PROTEIN ABJAS-COMPLEX (GIP. BINDINGEFFECTOR), G PROTEIN, EFFECTOR, RABODE, S SYMAPTIC EXOCYTORIS, RAB PROTEIN,	KABSA, KABFILLIN HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, AI F3. HYDROL ASF	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	ACETYLATION RNASE INHBITOR, RIBONUCLEASEANGIOGENIN INHBITOR ACETYLATION, LEUCINE-RICH REPEATS	HYDROLASE ORTHOPHOSPHORIC MONOESTER PHOSPHOTYDROLASE; PHOSPLOASE, ACETYLATION, TYROSINE PHOSPHATASE
Coumpound		PSO-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B.	RAB3A; CHAIN: A;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	LOW MOLECULAR WEIGHT PHOSPHOTYROSYL PHOSPHATASE; CHAIN: NULL;
SEQFOL D score		70.72	93.30	77.06	102.45	56.47	214.70
PMF							
Verify							
Psi Blast		1.4e-51	1.7e-63	3.4e-50	6.80-65	1.7e-52	1.4e-54
END AA		216	226	230	221	324	140
STAR T AA		15	64	20	47	2	2
CHAI N ID		æ	A	Ą	∀		
EDB EDB		ltx4	Izbd	2ngr	3rab	26nh	Spnt
SEQ NO:		1114	1114	1114	1114	1116	1120

1127 146h B 468 739 1.76-76 B 500 B							
Pub CIAA STAR END Pub Bast Verify Puff Stoppol.	PDB annotation	LIPID TRANSPORT APO A-1; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCIEROSIS, HDI, LCAT- ACTIVATION	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTEMA	COMPLEX (SERINE PROTEASENHHEITOR) PROTEASENHHEITOR (DELTAFEK)DENALPHAI; BGRCMK; SERINE PROTEASE, FIBRINGLYTIC BRYATMES, PLASMINGGEN 2 ACTIVATORS	COMPLEX (SERINE PROTEINASE/INHIBITOR)	COMPLEX (BLOOD) COAGULATION/INHIBITOR) HYDROLASE, STRINE HYDROLASE, STRINE PROTEINASE, PLASMA CALCTUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD)	HYDROLASEHYDROLASE NUBITOR ENTERORINASE, HEAYY CHAN; ENTERORINASE, LICHT CHAN; ENTEROPETIDASE, TRYPEINOGEN ACTIVATION, 2 HYDROLASEHYDROLASE
PDB CIAA STAR END Pa Blast Verify PMF	Coumpound	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	BETA-TRYPTASE; CHAIN: A, B, C, D;	PLASMINOGEN ACTIVATOR; CHAIN: A; GLU-GLY-ARG CHOROMETHYL KETONE; CHAIN: I;	ALPHA-THROMBIN; IAHT 4 CHAIN; L, H; 1AHT 5 HIRUGEN; 1AHT 8 CHAIN; I; 1AHT 9	ACTIVATED PROTEIN C. CHAIN: C. L. DPHE-PRO-MAI; CHAIN: P.	ENTEROPEPTIDASE; CHAIN: A; BNTEROPEPTIDASE; CHAIN: B; VAL-ASP-ASP-ASP-ASP-IYS PEPTIDE; CHAIN: C;
PB CHAI STAR END F9 Blast Verify 10	SEQFOL D score	51.65	100.75	106.52	91.53	99.33	89.82
PB CHA STAR END F9 Blast	PMF						
PDB CIAAI STAR END D N D TAA AA AA AA AA AA AA	Verify						
PDB CHAI STAR DD	Psi Blast	5.1e-05	3.4e-76	5.Ie-67	I.5e-73	5.1e-68	1.7e-76
PB CHAI IBVI A IBVI B IBVI B	END	280	741	739	744	739	739
1938 1841	STAR T AA	8	465	454	465	464	898
	CHAI	A	∢	. <	I	U	а
NO:	FDB UD	lavl	Ia0l	IaSi	laht	laut	1ekb
	SEQ O O	1122	1127	1127	1127	1127	1127

PDB annotation		COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE, PPACK, 2 CHOROMETHYLKETONE, COMPLEX (PROTEASE/INHIBITOR)	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)	COMPLEX (BLOOD COAGULATION/PROBAZYME) COAGULATION/PROBAZYME), COAGULATION/PROBNZYME), THROMBIN', 2 PRETRICOMBIN'2, PLASMA, SIRRINE PROTEASE	TERNARY COMPLEX (ZYMOGEN) TC, PCPA-TC; TERNARY COMPLEX (ZYMOGEN), SIRINE PROTEINASE, C-TERMINAL 2 PEPTIDASE	SERINE PROTEASE (TC)-T-P4; SERINE PROTEASE, FIBRINOLYTIC ENZYMES	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX
Coumpound	HYDROLASE(SERINE PROTEINASE) EPSILON- THROMBIN (E.C.3.4.21.5) NON- COVALENT COMPLEX WITH IETR 3 MQPA IETR 4	COAGULATION FACTOR XA- TRYPSIN CHIMERA; CHAIN: A; D-FHE-PRO-ARG. CHLOROMETHYLKETONE (PPACK) WITH CHAIN: I:	FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	ALPHA-THROMBIN; CHAIN; K; H; PRETHROMBIN-2; CHAIN; K;	PROCARBOXYPEPTIDASE A; CHAIN: A, B; PROFROTEINASE B; CHAIN: C; CHYMOTEXYPSINOGEN C; CHYMOTEXPSINOGEN C; CHAIN: D;	TWO CHAIN TISSUE PLASMINOGEN ACTIVATOR; CHAIN: A, B;	DNA; CHAIN: A, B, B, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
SEQFOL D score	92.09	89.40	98.96	93.49	95.69	102.89	71.69
PMF							
Verify score							
Psi Blast	1.5e-71	I.4e-76	3.4e-70	1.7e-72	1.5e-75	1.7e-68	6.8e-47
END	745	742	745	739	739	740	430
STAR T AA	465	463	465	425	454	467	342
CHAI	ш	¥.	H	M	Ω	ш	O
EDB EDB	letr	Ifry	ikig	1mkx	lpyt	Inf	Imey
SEQ NO:	1127	1127		11127		1127	1135

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PDB annotation	(ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TEITLA, SE GENE; NIRK, TEITLA, PROTEIN, DNA, TRANSCREPTION FROTEIN, DNA, TRANSCREPTION PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCREPTION)	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLY MERCASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGILATION/DAY) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELBERNT, YY1, ZINC2 FINGER PROTEIN, DAY-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGILATION/DAA)	COMPLEX (DNA-BÍNDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	HYDROLASE ATP SYNTHASE, FOFI- ATPASE, OXIDATIVE PHOSPHORYLATION, 2 MITOCHONDRIA, HYDROLASE
Coumpound		TRANSCRIPTION FACTOR IIIA, CHAIN: A, 58 RNA GENE; CHAIN: E, F.	TFIIIA; CHAIN: A, D; 5S RIBOSOMAI, RNA GENE; CHAIN: B, C, E, F;	YYI; CHAIN; C; ADENO- SEGOCIATED VIRUS 23 NITIATOR ELEMENT DIM; CHAIN: A, B;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	FI-ATPASE ALPHA CHAIN; CHAIN: A; FI-ATPASE BETA CHAIN; CHAIN: B; FI-ATPASE GAMMA CHAIN; CHAIN: G;
SEQFOL D score		67.88	105.09	80.44	202.77	64.40
PMF						
Verify score						
Psi Blast		1.5e-21	3.4e-41	1.7e-30	1.4e-60	1.7c-46
END		433	454	400	431	183
STAR T AA		342	276	277	277	-
CHAI N ID		⋖	<	ပ	<	æ
PDB IID		£	1416	lubd	2gli	1mab
SEQ ID NO:		1135	1135	1135	1135	1139

PDB annotation	HYDROLASE ATP SYNTHASE, FOFI- ATPASE, OXIDATIVE PHOSPHORYLATION, 2 MITOCHONDRIA, HYDROLASE	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD	TRANSCRIPTION INHIBITOR BETA- PROPELLER	TRANSCRIPTION INHIBITOR BETA- PROPELLER	COMPLEX (GTP. BRDINGTATANSDICER) BETA1, TRANSDICH BETA SUBURIT, GAMMA, TRANSDICH GAMMA SUBUNT; COMPLEX (GTP. BRDINGTANSDICER), BROTEIN, HETROTRIMER 2 SIGNAL, TRANSDICTION	MEMBRANE PROTEIN CRYSTAL STRUCTURE, MEMBRANE, FERM DOMAIN, TAIL DOMAIN	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUMCALMODULIN	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
Coumpound	FI-ATPASE ALPHA CHAIN; CHAIN; A; FI-ATPASE BETA CHAIN; CHAIN; B; FI-ATPASE GAMMA CHAIN; CHAIN; G;	TOLB PROTEIN; CHAIN: A;	TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	GT-ALPHAGIGAN,PHA GT-ALPHAGK, GFAINE, A; GT- BETA, GTAINE, B; GT-GAMMA; GHAIN: G;	MOESIN; CHAÎN: A, B; MOESIN; CHAÎN: C, D;	CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE; CHAIN: NULL:	CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE; CHAIN: NULL;
SEQFOL D score	130.11						329.67	
PMF		0.17	0.94	0.18	0.40	1.00		1.00
Verify score		0.19	0.70	0.16	0.01	0.69		0.64
Psi Blast	6.8e-66	1.6e-09	3.2e-29	3.2e-10	8e-22	1.4e-97	0	0
END	264	122	127	82	122	326	339	334
STAR	51	3	=	9	9	43	36	9
CHAI N ID	В	V	¥	A	m	4		
EDB EDB	Imab	lorz	lerj	lerj	lgot	lefi	Ia06	Ia06
SE SE	1140	1148	1148	1148	1148	1149	1153	1153

PDB annotation	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-I PROTEINS, 2 PLANT DEFENSE	PATHOGENESIS-RELATED RECIEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR. I PROTEINS, 2 PLANT DEFENSE	SIGNALING PROTEIN P21-RACZ; RHO GDI Z, RHO-GDI BETA, LY-GDI; BETA SANDWHICH, PROTEIN- PROTEIN COMPLEX, G-BOMAIN, 2 MANINGGLOBULIN FOLD, WALKER FOLD, GTP-BINDING	KINASE UMPICAP KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, MNW KINASE; PHOSPHORYL J TRANSFER, TRANSFINON STATE ANALOG COMPLEX TRANSFERASE	TRANSFERASE TRANSFERASE (PHOSPHORYL)	TRANSFERASE TRANSFERASE (PHOSPHORYL)	
Coumpound	PATHOGENESIS-RELATED PROTEIN P144; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	RAS-RELATED G3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;	URIDYLMONOPHOSPHATE/CY TIDYL,MONOPHOSPHATE KINASE, CHAIN: A;	PHOSPHOGLYCERATE MUTASE: CHAIN: A. B:	PHOSPHOGLYCERATE MUTASE; CHAIN: A, B;	TRANSFERASE(PHOSPHOTRA NSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4
SEQFOL D score	82.01					63.00	
PMF		1.00	1.00	0.62	1.00		99.0
Verify		0.47	0.06	-0.03	0.47		-0.17
Psi Blast	1e-28	16-28	1.2e-46	1.5e-19	5.1e-47	5.1e-47	3.4e-26
END	203	203	96	239	424	449	236
STAR	21	22	-	23	249	250	36
CHAI N ID			4	4	¥	¥	
EDB CI	Icfe	lcfe	1ds6	6Jb1	Iqhf	Jqb1	3adk
SEQ NO.	1155	1155	1156	1159	1159	1159	1159

PDB annotation			KINASE KINASE, PHOSPHOTRANSFERASE	COMPLEX (ZINC FINGERIDNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGERDNA)	COMPLEX (TRANSCRIPTION REGULATION/DAYA) COMPLEX (TRANSCRIPTION) REGULATION/DAYA), RNA REGULATION/DAYA), RNA POLYMERASE III, ETANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRETTON REGULATIONDAN PING-YAND I; TRANSCRETON INTIA,TION, INTIA,TONE ELEMENT, YYI, ZINC 2 FINGER PROTEIN, DNA-RROTEIN RECOGNITON, 3 COMPLEX (TRANSCRETTON)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-
Coumpound	TRANSFERASE (PHOSPHORYL) PHOSPHOGLYCERATE MUTASE (B.C.2.7.5.3) DE- PHOSPHO ENZYME 3PGM 4	TRANSFERASE (PHOSPHORYL) PHOSPHOGLYCERATE MUTASE (E.C.2.7.5.3) DE- PHOSPHO ENZYME 3PGM 4	THYMIDYLATE KINASE; CHAIN: A, B, C, D, E, F, G, H;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAI. RNA GENE; CHAIN: B, C, E, F;	YYI; CHAIN; C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN; A, B;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D score		58.96		100.83	108.88	86.63	98.31
PMF	00.1		0.19				
Verify	0.19		-0.13				
Psi Blast	1.7e-48	1.7e-48	1.2e-29	4.8e-51	8e-38	5.1e-53	3.2e-34
END AA	14	14	237	442	437	442	443
STAR T AA	249	249	34	360	276	334	304
CHAI			V	υ ·	∢	ပ	V
804 01	3pgm	3pgm	3tmk	Imey	1116	Iubd	2gli
SEQ B SQ	1159	1159	1159	1160	1160	1160	1160

PDB annotation	BINDING PROTEIN/DNA)	KINASE KINASE, SIGNAL TRANSDUCTION,	TRANSFERASE TRANSFERASE, SERINETHREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SERITHR KINASE.	ROTEIN KINASE CDK2; PROTEIN PROSE CELL CYRES, CELL DIVISION, MITORIS, CELL CONDES, CELL DIVISION, MITORIS, INHEITION CORRES, FIDINES, CYCLIN CORRES, POWER, CYCLINES, CYCLIN DEPRODENT KINASE INHEITION, DEPRODENT KINASE INHEITION, CORRES, CYCLIN CO	HEADER HELLX COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR
Coumpound	B	CALCIUM/CALMODULIN- KDEPENDENT PROTEIN KINASE; T	SE CK2/ALPHA-	THAN NEEDER SPECIPIOST IN THAN SEEDER SPECIPIOST IN SPECIPIOS IN SPECI	CYCLIN-DEPENDENT KINASE C 6; CHAIN: A; P19INK4D; CHAIN: P
SEQFOL D score		130.42	108.45	111.26	113.75
PMF					
Verify					
Psi Blast		3.2e-84	6.8e-54	4.8e-56	6.8e-62
END		340	334	348	331
STAR		43	18	50 50	47
CHAI				ш <	۷ ,
PDB		1a06	lafo	lapm Iaq1	1bk
SEQ El Sign		1163	1163	1163	1163

PDB annotation	PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE			PHOSPHOTRANSEERSE FORRIK, FIBRODILAST GROWTH FACTOR RECEPTOR I; TRANSFERASE, TYROSING-PROTEIN KINASE, APP- BINDING, 2-PHOSPHORYLATTON, RECEPTOR, PHOSPHOTRANSERASE	PHOSPHOTANSEERSE FORRIK, FIBROBLAST GROWTH FACTOR RECEPTOR I, ITANSFERASE, TYROSINE-PROTEIN KINASE, AIP- BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSEERASE	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN
Coumpound	B;	C-TERMINAL SRC KINASE; CHAIN: A;	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK 3 (E.C.2.7.1.37) ICMK 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAND- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP 3 (CATALYTIC SUBUNIT) ICTP 4	FGF RECEPTOR 1; CHAIN: A, B;	FGF RECEPTOR 1; CHAIN: A, B,	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;
SEQFOL D score		93.49	175.36	168.10	106.44	117.87	128.78
PMF							
Verify							
Psi Blast		1.3e-31	0	0	6.4e-31	1.3e-37	1e-66
END		300	353	343	309	304	348
STAR T AA		4	6	15	33	36	20
CHAI N ID		V	ш	ш	∢	g	
PDB		Ibyg	lcmk	letp	Ifgk	1fgk	Ihcl
SEQ No. 13		1163	1163	1163	1163	1163	1163

PDB annotation	KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION	COMPLEASE COMPLEASE TYROSINE KINASE, SIGNAL TRANSDUCTION, TRANSPERASE, TRANSPERASE, TRANSPERASE, TRANSPERASE, TRANSPERASE, TRANSPERASE, TRANSPERASE, TRANSPERASE, TRANSPERATION TRANSPERATIO	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINETHREONINE-PROTEIN KINASE, 2 298	KTANSE KABBIT MUSCLE PHOSPHORYT, ASE KINASE; GLYCOGEN METABOLISM, TRANSFRASE; BERNETHREONINS-PROTEIN, 2 KTANSE, ATTE BINDING CALMODULIN-BINDING	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE	SERINE KINASE SERINE KINASE,
Соимроинд		INSULIN RECEPTOR; CHAIN: B;	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TWITCHIN; CHAIN: A, B;	MAP KINASE P38; CHAIN: NULL;	PHOSPHORYLASE KINASE; CHAIN: NULL;	ERK2; CHAIN: NULL;	TITIN; CHAIN: A, B;
SEQFOL D score		99.07	104.42	159.16	109.88	156.26	104.21	131.84
PMF								
Verify								
Psi Blast		3.2c-26	5.1e-64	1c-90	1.6e-50	1.1e-83	9.6e-46	8e-57
END		323	388	359	395	305	389	370
STAR		86	38	24	31	49	44	47
CHAI		₽.		₹				Ą
E C C C C C C C C C C C C C C C C C C C		EEE	Ijnk	Ikob	1p38	1 phk	1рте	1tki
SEQ US		1163	1163	1163	1163	1163	1163	1163

		,			
TITIN, MUSCLE, AUTONHIBITION TRANSFEASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERNIPITEDONINESPROTEIN KINASE MAP KINASE APREZ	IMMUNE SYSTEM IMMUNOGLOBULIN, INMUNORECEPTOR, IMMUNE SYSTEM	T-CELL SURFACE GLYCOPROTEIN MAUNOGOLOBILIN POLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL, SURFACE GLYCOPROTEIN, T-CELL SURFACE GLYCOPROTEIN	IMMUNE SYSTEM FAB 58.2; FAB 58.2; V3.LOOP; IMMUNGGLOBULIN; FAB, HIV-I, GP120, V3, IMMUNE SYSTEM		IMAUNE SYSTEM HUMAN TCRPEPTIDEMHC COMPLEX, HIA- A2, HTLV-1, TAX, TCR, T 2 CELL RECEPTOR, IMMUNE SYSTEM
EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	ALPHA-BETA T CELL RECEPTOR (TCR) (D10); CHAIN: A;	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	1GGI ANTIBODY 58.2 (LIGHT CHANN; CHANE: L; IGGI ANTIBODY 32.2 (HEAVY CHANN; CHANN: H; EXTERIOR MEMBRANE GLYCOROTEIN(GP120);	IMMUNOGLOBULIN IMMUNOGLOBULIN GI (KAPPA LIGHT CHAIN) FAB' FRAGMENT IFIG 3	MHC CLASS I HLA-A; CHAIN: A; BETA-Z MICROGLOBULIN; CHAIN: B; TAX PEPTIDE P64; CHAIN: C; HMAN T-CELL RECEPTOR; CHAIN: D; HLA-A 0201; CHAIN: F
116.38	50.07	30.90	51.50	51.43	50.17
			•		
3,4e-69	1.6e-12	0.00034	4.8e-21	8e-19	6.4e-23
400	247	190	244	239	219
36	17	ជ	11	11	14
	< <		Ħ	н	Д
3erk	1bw m	ledy	1158	lfig	lqm
1163	1170	1170	1170	1170	1170
	3erk 36 400 3.4e-69 116.38 EXTRACELLULAR RECULATED KINASE 2; CHADR: NULL;	3erk 36 400 3.4e-69 116.38 BXTRACELLULAR RECULATED KINASE 2; CHAIN: NULL; CHAIN: NULL; 1bw A 17 247 1.6e-12 30.07 ALPHA-BETAT CELL m A; CHAIN: NULL; A; A; A;	36 400 3.4e.69 116.38 EXTRACELLULAR RECUIATED KINASE 2; CHADR: NULL; CHADR: NULL	36 400 3.4-69 116.38 EXTRACELLULAR	16.38 EXTRACELLULAR

Coumpound PDB annotation	IMMUNOGLOBULIN IGGZA FAB FRAGMENT (CN1206) 2GFB 3	IMMUNOGLOBULIN; CHAIN: A, IMMUNOGLOBULIN B, C, D;	SERINETHREGOINE PROTEIN HYDROLASE TETRATRICOPEPTIDE, PHOSPIAITASE 5, CHAIN: THE HYDROLASE, PROSPINEMENTONS, PROTEIN-PROCTEIN TREACTIONS, TREACTIONS STRUCTURE		GAMMA-FIBRINGGEN BLOOD COAGULATION FACTOR CARBOXYL TEAMINAL BLOOD COAGULATION, GLYCOPROTEIN CALCIUM, PLACE PLAIN: NULL, ALTEREY LASMA, 2 ALTERA VICTOR SOLICING.	DISEASE MUTATION, 3 POLYMORPHISM	CHAIN: A, B, C, D, E, F,			
MMUNOGLOBUI FAB FRAGMENT	2	IMMUNOGLOBUI B, C, D;	SERINE/THREONI PHOSPHATASE 5; NULL;		GAMMA-FIBRING CARBOXYL TERN	FRAGMENT; CHA	FRACMENT; CHA FIBRIN; CHAIN: A G, H, I, J;	FRAUMENI; CHAN FIBRN; CHAIN: A G, H, I, J; FIBRN; CHAIN: A G, H, I, J;	FRAUMENI; CHAIN: A G, H, LJ; FIBRIN; CHAIN: A G, H, L, J; FIBRINOGEN-420; C, D, E, F, G, H;	PRAUMENT, CHAINE G. B. L. J.; FIBRIN, CHAINE A. G. B. L. J.; FIBRING CEATHE A. G. B. L. J.; FIBRINGOEN-420, G. D. E. F. G. H. FIBRINGOEN; CH. D. F. F. S. T. M. N. I.
D score	51.08	51.13			129.15		132.32	132.32	132.32 141.90 154.36	132.32 141.90 154.36 141.24
PMF			90:04	L						
Verify			-0.20							
Psi Blast	1.6e-17	9.6e-21	0.0017		1.7e-53		1.7e-63	1.7e-63 3.4e-62	3.40-63 3.40-62 1.70-57	3.4c-63 1.7c-57 1.7c-57
END	240	239	245		418		416	416	416	416 422 419 419
STAR	15	17	152		561		148	148	148	148 151 242 170
CHAI N ID	V	В					м	a v	м U 4	м С 4 С
P 08	2gfb	2pcp	IaI7		ij.		1fzc	lfzc 1fzc	lfzd	lfzc Iffzd Iffzg
SEQ NO:	1170	1170	1174		0811		1180	1180	1180	1180

SEO	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
ΘŸ	8	e e	TAA	¥		seore	score	D score		`
									D, E, F, S, T, M, N;	COAGULATION, PLASMA, PLATELET, FIBRINOGEN, FIBRIN
1811	1fm		2	104	1.6e-43			145.02	MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: NULL;	CYTOKINE MACROPHAGE, INFLAMMATORY RESPONSE, CYTOKINE
1181	lgif	¥	-	115	1.6e-52			180.54	GLYCOSYLATION-INHIBITING FACTOR; CHAIN: A, B, C;	CYTOKINE MACROPHAGE, INFLAMMATORY RESPONSE, CYTOKINE
1811	lmfi	V	2	115	3.2e-52			170.94	MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: A, B, C;	CYTOKINE PHENYLPYRUVATE TAUTOMERASE; CYTOKINE, MACROPHAGE, INFLAMMATORY RESPONSE, TAUTOMERASE
1185	IdZn	∢	195	450	1,2e-35			76.43	N-ETHYLMALEIMIDE- SENSTIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
1195	1a8y		382	723	4.8e-25			91.59	CALSEQUESTRIN; CHAIN: NULL	CALCIUM-BINDING PROTEIN CALSEQUESTRIN, CALCIUM- BINDING PROTEIN, SARCOPLASMIC 2 RETICULUM, RABBIT SKELFTAL MUSCLE
1200	layz	٧	31	061	3.2e-47			71.29	UBIQUITIN-CONJUGATING ENZYMB RAD6; CHAIN: A, B, C;	UBIQUITIN CONUGATION UBC2; UBIQUITIN CONUGATION, UBIQUITIN-CONUGATING ENZYME
1200	lc4z	D	47	161	9.6e-40			84.49	UBIQUITIN-PROTEIN LIGASE	LIGASE E6AP; UBCH7; BILOBAL
									E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING	STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2
	Ī								ENZYME EZ; CHAIN: D;	UBIQUITIN CONJUGATING ENZYME
1200	Idcd	∢ _	4	193	3.2e-53			81.61	UBIQUITIN CONJUGATING ENZYMB; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN- CONJUGATING ENZYME, YEAST

PDB annotation	UBIQUITING-CONUGATING ENZYME UBIQUITING- CONUGATING ENZYME; UBIQUITING-CONUGATING ENZYME, UBIQUITING-LINGECTED 2 PROTECLY SIS, CELL CYCLE CONTROL, LIGASE	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THOESTER 2 BOND, LIGASE	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST	TRANSFBRASE IL-2-INDUCIBIE T- CELL KINASE; TRANSFBRASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE		TRANSFERASE TYROSINE-PROTEIN KINASE, TRANSFERASE, SIGNAL TRANSDUCTION, 2 SH3	COMPLEX (SH3 DOMAIN/VIRAL ENHANCER) SIC-HOMOLOGY 3 DOMAIN; COMPLEX (SH3 DOMAIN/VIRAL ENHANCER), PROTO-ONCOGENE, 2
Coumpound	UBC9; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONTUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	ITK; CHAIN: NULL;	BRUTON'S TYROSINE KINASE; CHAIN: NULL;	HEMOPOIETIC CELL KINASE; CHAIN: A, B, C, D, E, F;	FYN TYROSINE KINASE; CHAIN: A, C; HIV-I NEP PROTEIN; CHAIN: B, D;
SEQFOL D score	74.19	71.32	67.54	64.54				
PMF					90.0	0.58	0.21	0.82
Verify					-0.35	0.55	0.03	0.12
Psi Blast	1.6e-43	3.2c-47	1.4e-41	3.2e-43	3.2e-15	1.1e-13	4.8e-15	1.6e-17
END	193	193	193	193	317	319	318	317
STAR T AA	24	31	26	33	241	250	258	258
CHAI N ID	∢						¥	<
EDB EDB	Reu Iu9a	2aak	2e2c	2ncz	lawj	1aw <i>w</i>	IbuI	lefi
SEQ NO.	1200	1200	1200	1200	1204	1204	1204	1204

PDB annotation	PROTEIN KINASE, PHOSPHORYLATION, 3 AIDS, MYRISTYLATION, CIP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPII HELIX, PXXP MOTTE	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO- ONCOGENE, TRANSFERASE, TYROSINE-RROTENKINASE, TYROSINE-RROTENKINASE, PHOSPHORYATION, AFP BRUDNG, MYRISTYLATION, SH3 DOMAIN, 3 COMPILEX COMPILEX		COMPLEX (TRANSTERASE/PEPTIDE) SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSTERASE/PEPTIDE)	TYROSINE-ROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSEREAKSE, TROSINE- PROTEIN KINASE, PROTEIN KINASE, PROTEIN KINASE, PROMAIN	
Coumpound		PHOSPHOTRANSTERANE FYN; CHAIN: A; 38P-2; CHAIN: B;	PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (RECEPTOR-BOUND PROTEIN 2 (RESEX ATTERNAL I (BBR 3 SH3 DOWALD), COMPLEXED WITH SOS-A PEPTIDE I (BR 4 (NMR, 29 STRUCTURES) I (BR 5	G-SRC; CHAIN: C; NLJ (MN7- MN2-MN1-PLPPLP); CHAIN: N;	TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	PHOSPHOTRANSFERASE FYN
SEQFOL D score						
PMF		0.58	0.63	0.69	0.43	0.31
Verify score		0.32	0.25	0.42	0.41	0.39
Psi Blast		6.4e-19	4.8e-12	1.3e-16	4.8e-13	8e-19
END		318	322	316	318	318
STAR		255	260	259	257	256
CHAI N ID		⋖	Α	υ υ	∢	A
EDB ED		Ifyn	1gbr	Info	lqly	Ishf
SEQ B B SEQ		1204	1204	1204	1204	1204

PDB annotation		TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE	ELECTRON TRANSPORT HELIX, BETA-STRAND, ELECTRON TRANSPORT		COMPLEX (HYDROLASZINHIBITOR), LDTI; COMPLEX (HYDROLASENHIBITOR), HYDROLASE, INHIBITOR, 2 INELAMMATION, TRYPTASE	CALCUM-BINDING PROTEIN CALMODULIN CRUUM TRIC- DOMAIN, RESIDUES 1 - 75; CERUM- LOADED, CALCUM-BINDING PROTEIN	METAL BINDING PROTEIN CAVP;
Соитроип	PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) ISHF 3 (SH3 DOMAIN) 1SHF 4	ÁBL TYROSINE KINASE; CHAIN: NULL;	HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	CYTOCHROME BS; CHAIN: A;	COMPLEX(SERINE PROTEIN-ASE, PHEBITOR) ALPHA-CHYMOTRYPEIN (B.C.3.4.21.1) COMPLEX WITH TURKEY 1 CHO 4 OYOMUCOID THIRD DOMAIN (OMITKYSS) 1CHO 5	TRYPSIN; CHAIN: T, TRYPTASE INHIBITOR; CHAIN: L;	CALMODULIN; CHAIN: NULL;	CALCIUM VECTOR PROTEIN;
SEQFOL D score								
PMF		-0.15	0.55	0.19	0.58	0.86	0.05	0.23
Verify score		0.04	0.04	69.0	-0.30	-0.23	-0.15	-0.50
Psi Blast		9.6e-28	3.2e-15	0.0096	5.1e-07	1.7e-07	3.4e-05	6.8e-06
END		423	318	86	592	587	410	410
STAR T AA		251	255	38	554	559	356	349
CHAI N ID				V	_	1		V
PDB ID		2abí	4hck	loxy	Icho	Ildt	lak8	1c7w
SEQ ID NO:		1204	1204	1205	1208	1208	1215	1215

PDB annotation	EF-HAND FAMILY, CALCIUM BINDING PROTEIN, NMR	-		STRUCTURAL PROTEIN HELIX- TURN-HELIX	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER	ANTIPREEZE PROTEIN INSECT ANTIPREEZE PROTEIN, THERMAL HYSTERESIS, TENEBRIO 2 MOLITOR, IODINATION, RIGHT- HANDED BETA-HELX, TMAFP	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE	BLOOD CIOTING COMPLEXGERINE PROTEAGE/COFACTORALIGAND), BLOOD COAGULATION, 2 SERINE PROTEAGE, COMPLEX, CO-FACTOR, REGEPTOR ENTYME, 3 NHBITOR, GLA, EGF, COMPLEX (SERINE 4
Coumpound	CHAIN: A;	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-BEFENDENT PROTEIN XINASE II ICDM 4	COMPLEX(SERINE PROTEIN-ASE-HUBITOR) A APPHA-CHYMOTTRYPEIN (B.C.3.4.21.1) COMPLEX WITH TURKEY 1CHO 4 OVOMUCOID THIRD DOMAIN (OMTKY3S) 1CHO 5	CARDIAC TROPONIN C; CHAIN: A;	CALMODULIN; CHAIN: A;	THERMAL HYSTERESIS PROTEIN ISOFORM YL-1; CHAIN: A, B;	CALMODULIN; CHAIN: A;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;
SEQFOL D score								
PMF		60:0	0.65	0.21	0.05	0.13	0.69	-0.19
Verify		-0.48	0.04	-0.26	0.15	0.21	0.10	0.07
Psi Blast		3.4e-05	5.16-10	1.7e-05	1.4e-05	3.2e-06	6.8e-05	4.8e-09
END		818	ž	410	414	305	410	302
STAR T AA		356	39	349	348	226	349	236
CHAI N ID		∢	<u>.</u>	٧	¥	∢	V	J
PDB EI		ledm	1cho	ldtl	lexr	lezg	1771	1fak
SEQ NO P		1215	1215	1215	1215	1215	1215	1215

PDB annotation	PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING	RETRIEGELLU-AN MODULE OSTEDNECTIN, SPARC, SECRETED PROTEIN ACIDIC AND EXTRACELLU-AN MODULE, GLYCOPROTEIN, ANTI-ADRESIVE PROTEIN A. SOLLAGEN BINDING, STITE-DIRECTED, MUTAGENESIS, GLYCOSYLATED 3 PROTEIN	GROWTH FACTOR EH1; EH GROWTH FACTOR EH1; EH DOMAIN, EPS15, EF-HAND, SOLUTION STRUCTURE, S100 PROTEIN		COMPLEX (SERINE PROTEASE/NIED SGPE, 1SGP PROTEASE/MHIBITOR) SGPE, 1SGP 14 SERINE PROTEINASE, PROTEIN INHIBITOR 1SGP 25	CALCIUM-BINDING PROTEIN BM- 40, OSTEONECTIN; ISRA 7 EXTRACELLULAR MATRIX PROTEIN ISRA 20	CALCIUM-BINDING PROTEIN BM- 40, OSTBONECTIN; ISRA 7 EXTRACELLULAR MATRIX PROTEIN ISRA 20	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2
Coumpound		BASEMENT MENGRANE PROTEIN BM-40; CHAIN: A, B;	EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CHAIN: A;	CALCIUM-BINDING PROTEIN RAT ONCOMODULIN 1RRO 3	STREPTOMYCES GRISEUS PROTEINASE B; 1SCP 6 CHAIN: E; 1SCP 7 TURKEY OVOMUCOID INHIBITOR; 1SCP 11 CHAIN: I; 1SCP 12	SPARC; 1SRA 4 CHAIN: NULL; 1SRA 5	SPARC, ISRÁ 4 CHÁIN: NULL; ISRA 5	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;
SEQFOL D score		73.86					58.51	
PMF			0.01	61.0	0.55	0.72		-0.19
Verify			-0.05	-0.37	0.67	0.43		0.09
Psi Blast		1.7e-28	6.8e-07	3.4e-05	1.7e-08	1.5e-38	1.5e-38	4.8e-09
END		426	419	410	\$ 8	423	426	313
STAR T AA		201	348	348	43	279	279	240
CHAI N ID		∢	<		I			ı
PDB U		Inub	lgit	Irro	Isgp	1sra	1sra	Ixka
SEQ No.		1215	1215	1215	1215	1215	1215	1215

PDB annotation	GROWTH FACTOR LIKE DOMAIN				PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN; MEMBRANE 2 BINDING PROTEIN	PHOSPHOLIPID ANALOG PLACRIVTAL ANTICOGAGULANT PROTEIN, PHOSPHOLIPID ANALOG, CALCTUM BINDING PROTEIN, MEWBRANE 2 BINDING PROTEIN					
Coumpound		PROTEINASE INHIBITOR (KAZAL) OVOMUCOID THIRD DOMAIN CLEAVED RDI 30VO 3	CALCIUM-BINDING PROTEIN PARVALBUMIN (ALPHA LINEAGE) 5PAL 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	ANNEXIN V; CHAIN: NULL;	ANNEXIN V; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I JAIN 3	CALCIUM/PHOSPHOLIPID- BINDING PROTEIN ANNEXIN V IALA 3	CALCIUM/PHOSPHOLIPID- BINDING PROTEIN ANNEXIN V IALA 3
SEQFOL D score						75.48		170.55			75.25
PMF		0.21	0.13	-0.19	1.00		00'1		00.1	1.00	
Verify		92.0	-0.11	0.08	0.58		0.23		-0.02	0.42	
Psi Blast		1.7e-09	3,4e-05	3.2e-15	3.2e-51	3.2e-51	le-68	1c-68	4.8e-67	3.2e-53	3.2e-53
END		84	410	286	217	217	222	223	222	214	214
STAR		04	348	112	-	-	19	61	62	-	-
CHAI N ID				A							
PDB ID		30vo	Spai	вВм6	la8a	1a8a	lain	lain	lain	lala	Iala
SEQ ID NO:		1215	1215	1215	1216	1216	1216	1216	1216	1216	1216

PDB annotation	CALCIUMPHOSPHOLIPID-BINDING PROTEIN 22.5 KO CALELECTRIN, ENDONEXIN I, LANN 73.5 KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12.2 CHROMOBINDIN IV, PROTEIN II LIANN 13	CALCIUMPHOSPHOLIPID-BINDING PROTEIN 23.5 KD CALEI-CTRIN, BENDONEXIN I, IANN 73.5 KD CALEI-CTRIN, IANN 73.5 KD CALEI-CTRIN, IANN 12.2 CHROMOBINDIN IV, PROTEIN II LIPOCORTIN IV, IANN 12.1	CALCIUMPHOSPHOLIFID-BINDING PROTBIN 32.5 KO CALELECTRIN, ENDONEXIN I, IANN 73.5KD CALELECTRIN, IANN 73.5KD CALELECTRIN, IANN 12.2 CHROMOBINDIN IV, PROTBIN II ILPOCORTIN IV, IANN 12.2	CALCIUMPHOSPHOLIPID-BINDING PROTEIN PRE, PROTEIN III, G-KDA- CALCIMEDIN, LIPOCORITIN ANDEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, CALCIUMPHOSPHOLIPID-BINDING	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN PRE, RENCTEIN III, GF.KDA- CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, CALCIUM/PHOSPHOLIPID-BINDING CALCIUM/PHOSPHOLIPID-BINDING
Coumpound	ANNEXIN IY; IANN 5 CHAIN: NULL; IANN 6	ANNEXIN IV; IANN 5 CHAIN: NULL; IANN 6	ANNEXIN IV; IANN 5 CHAIN: NULL; IANN 6	ANNEXIN VI; CHAIN: NULL;	ANNEXIN VI; CHAIN: NULL;
SEQFOL D score		68.51			
PMF	1.00		1.00	0.1	9.1
Verify	0.42		0.46	0.24	0.48
Psi Blast	9.6e-51	3.2e-67	3.2e-67	1.6e-50	9.6e-78
END	215	216	219	216	221
STAR T AA	=	_	29	10	kn .
CHAI N ID					
FDB TD	lann	lann	Iann	Iavc	lavc
SEQ NO:	1216	1216	1216	1216	1216

PDB annotation	PROTEIN	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY IAXN 14	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14		PHOSP HOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN				
Coumpound		ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	BINDING ANNEXIN V BINDING ANNEXIN V BINDING ANNEXIN V IL PLACENTIAL IHVD 3 ANTICOAGULAN PROTEIN MUTATION IHVD 4 WITH GLU MUTATION IHVD 4 WITH GLU IHVD 5	ANNEXIN V; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN 1 IAIN 3	CALCTUM/PHOSPHOLIPID BINDING ANNEXIN 1 1AIN 3	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN 1 IAIN 3	CALCIUM/PHOSPHOLIPID- BINDING PROTEIN ANNEXIN V 1ALA 3
SEQFOL D score			84.90		69.28			403.43		
PMF		1.00		00.1		1.00	1.00		00:1	1.00
Verify		0.76		0.70		0.64	0.22		0.17	0.31
Psi Blast		9.6e-53	3.2e-67	3.2e-67	1.1c-49	8e-39	8e-32	0	0	3.2e-38
END		216	223	222	212	189	187	304	300	186
STAR T AA		4	53	59	-	∞ .	13	33	35	8
CHAI N ID										
EDB EDB		laxn	laxn	Iaxn	Ihvd	1a8a	Iain	lain	lain	lala
SEQ NO:		1216	1216	1216	1216	1217	1217	1217	1217	1217

PDB annotation	CALCIUM/PHOSPHOLIPID-BINDING PROTIEN 22. KND ACHE-LECTRIN, ENDONEXIN ; IANN 73.2KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IY, IANN 12.2 CHROMOBINDIN IY, PROTIEIN II IANN 13	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P88, PROTEIN III, G7-KDA- CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14		PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT
Coumpound	ANNEXIN IV; IANN 5 CHAIN: NUIL; IANN 6	ANNEXIN VI; CHAIN: NULL;	ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	CALCUMPACPHOLPID BINDING ANNEXIN V (LIPOCONTIN V, ENDOREXIN IL PLACENTIAL HYDD3 ANTICOAGULLANT PROTEIN) (CALCUM DONS ARE VISIBLE) MILTATION HYDA WITH GLU I? REPLACED BY GLY (EITO) HYDD3	ANNEXIN V; CHAIN: NULL;	ANNEXIN V; CHAIN: NULL;
SEQFOL D score					58.84	
PMF	1.00	1.00	1.00	1.00		1.00
Verify	0.55	0.28	0.54	0.31		9.08
Psi Blast	3.2e-38	4,8e-26	1.6e-37	6.4e-38	3.2e-66	3.2e-66
END	187	186	187	184	195	194
STAR T AA	·	«»		·	31	33
CHAI N ID						
en Gr	lann	lavc	laxn	Ihvd	laßa	la8a
SEQ El Ö	1217	1217	1217	1217	1218	1218

		г	Γ-	_			1	
PDB annotation	PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN				CALCUM/PHOSPHOLIPID-BINDING PROFIBER 3.2. KD CALEBECTRIN, ENDOWEXIN I, IANN 73.2.KD CALEBECTRIN, ENDONEXIN I, LIPOCORTIN IV, IANN 12.2 CHROMOBINDIN IV, PROTEIN II	CALCUM/PHOSPHOLIPID-BINDING PROFIERS 25. KD CALEBECTRIN, ENDONEXIN I; IANN 132.KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IY, IANN 12.2 CHROMOBINDIN IV, PROTEIN II IANN 13	CALCIUM/PHOSPHOLIPID-BINDING PROFIBIN P88, PROTEIN III, 67-KDA- CALCIMEDIN, LIPOCOKTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, CALCIUM/PHOSPHOLIPID-BINDING PROTEIN	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING,
Coumpound		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	ANDEXIN IV; IANN 5 CHAIN: NULL; IANN 6	ANDEXIN 1Y; IANN 5 CHAIN: NULL; IANN 6	ANNEXIN VI; CHAIN; NULL;	ANNEXIN VI; CHAIN: NULL;
SEQFOL D score			170.39		65.05			
PMF		00'1		1.00		1.00	1.00	1.00
Verify score		0.23		0.15		0.54	0.30	0.61
Psi Blast		1e-68	16-68	1.6e-65	3.2e-68	3.2e-68	1.6e-38	1.6e-71
END		194	195	194	195	190	186	193
STAR T AA		33	33	35	33	34	2	34
CHAI N ID								
PDB		lain	lain	lain	1ann	lann	Iavc	lavc
SEQ NO:		1218	1218	1218	1218	1218	1218	1218

PDB annotation	MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY IAXN 14	METAL BINDING PROTEIN PLANT ANNEXIN, CAPSICUM ANNUUM, BELL PEPPER, CALCIUM 2 BINDING PROTEIN			SCAPFOLD PROTEIN SCAFFOLD PROTEIN, PP2A,
Coumpound		ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	ANNEXIN 24(CA32); CHAIN: A, B;	BINDING ANEXIN V BONDING ANEXIN V BONDING ANEXIN V BONDING ANEXIN I PLACESTIAL HAVD S ANTICOAGULANT PROTEIN MATATION HAVD 4 WITH GLAL I REPLACED BY GLY (BIYO) HAVD 5	CACCIDIM/POSPIOLIPID BINDING ANNEXIN V BINDING ANNEXIN V BIL PLACEDINAL V BIL PLACEDINAL HVD B CALCING HOST CALCING HOST CALCING HOST HYD A WITH GLU HYD A WITH GLU HYD BY GLY (B176) HYD BY HYD HYD BY HYD HYD BY HYD HYD BY HYD	PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;
SEQFOL D score		85.90			68.02		120.56
PMF			00:1	1.00		00:1	
Verify score			0.70	0.02		0.59	
Psi Blast		6.4e-67	6.4e-67	3.2e-19	9.6e-68	9.6e-68	1.6e-45
END AA		195	194	691	195	194	627
STAR T AA		25	31	2	32	33	23
CHAI				¥			<
PDB ID		laxn	Iaxn	1415	1hvd	lhvd	1b3u
SEQ NO.		1218	1218	1218	1218	1218	1219

PDB annotation	PHOSPHORYLATION, HEAT REPEAT	RROTEN PHOSPHATASE PP2A; ROAFFOLD PROTEIN SCAFFOLD CHAIN: A, B; PHOSPHORYLATION, HEAT REPEAT	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN, ARM REPEAT	NUCCLEAR MAPORT RECEPTOR KARYOPHERNA ALPHA, NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, ATUDINIBITION, INTRASTERIC REGILATION	NUCCLEAR MADORT NECEPTOR KARYOPHERIN ALPHA, NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOMIBITION, INTRASTERIC REGULATION	SMALL GTPASE KAR YOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-
Coumpound		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO- ONCOGENE PROTEIN; CHAIN: C, D, E, F;	KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO- ONCOGENE PROTEIN; CHAIN: C, D, E, F;	IMPORTIN ALPHA; CHAIN: A;	IMPORTIN ALPHA; CHAIN: A;	RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	BETA-CATENIN; CHAIN: NÜLL;
SEQFOL D score						118.96			
PMF		0.23	-0.07	1.00	0.86		0.53	-0.15	90.0
Verify		0.07	90.04	0.36	0.57		0.50	0.01	0.51
Psi Blast		1.6e-09	1.6e-45	1.7e-10	1.4e-44	1.3e-43	1.3e-43	4.8e-15	1.1e-39
END		643	625	473	643	828	643	633	643
STAR T AA		320	71	211	279	179	272	318	239
CHAI N ID		∢	4	⋖	¥	¥	A	В	
EDB ID		1b3u	1b3u	lee4	lee4	lial	lial	libr	2bct
SEQ ID NO:		1219	1219	1219	1219	1219	1219	1219	1219

PDB annotation	CATENIN, STRUCTURAL PROTEIN	LL; ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON	A, OXIDOREDUCTASE FATTY ACID HYDROXYTASE, FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK	OXIDOREDUCTASE (OXYGENASE)	A. OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK	A. OXIDOREDUCTASE FATTY ACID HYDROXYLASE, FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P458 REMARK	OXDOREDUCINE PROGESTERONE 21- HYDROXYLASE, CYPICS P450 I, MEMERANE FORDEN, MCMERANE FORDEN, HYDROXYLASE, BERZOR(A) 2 FYRENE HYDROXYLASE, ESTADIOL 2-HYDROXYLASE, FSTADIOL 2-HYDROXYLASE, FSTADIOL 2-HYDROXYLASE, FSTADIOL 2-HYDROXYLASE,		OXIDOREDUCTASE (OXYGENASE)
Coumpound		BETA-CATENIN; CHAIN: NULL;	CYTOCHROME P450; CHAIN: A, B;	CYTOCHROME P450 ERYF; 10XA 5 CHAIN: NULL 10XA 6	CYTOCHROME P450; CHAIN: A, B;	CYTOCHROME P450; CHAIN: A, B;	CYTOCHROME 1450 2C5; CHAIN: A;	NITRIC OXIDE REDUCTASE; CHAIN: A;	CYTOCHROME P450 ERVF; 10XA 5 CHAIN: NULL 10XA 6
SEQFOL D score			174.17	94.76					
PMF		0.24			0.04	0.29	66:0	0.05	0.28
Verify		0.46			-0.20	-0.23	-0.02	-0.08	-0.40
Psi Blast		3.2e-35	9.6e-53	3.2e-24	1.3e-18	3.4e-36	3.26-92	1.7e-21	6.8e-33
END		643	486	486	324	318	325	318	318
STAR		277	61	27	35	19	31	48	61
CHAI			¥		∢	V V	<	¥	
PDB		3bct	1bu7	loxa	1bu7	1bu7	1dt6	1126	loxa
SEQ No.		1219	1221	1221	1222	1222	1222	1222	1222

		Γ.		,				
PDB annotation	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD	TRANSCRIPTION INHIBITOR BETA- PROPELLER	TRANSCRIPTION INHIBITOR BETA- PROPELLER	TRANSCRIPTION INHIBITOR BETA- PROPELLER	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT;	GAMMAI, TRANSDUCIN GAMMA SUBUNIT, COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETTER OTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (GTP. BINDINGTRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMAT, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP. BINDINGTRANSDUCER), G PROTITEN, HETEROTYRMER 2 SIGNAL, TRANSDUCTION	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-
Coumpound	TOLB PROTEIN; CHAIN: A;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA;	CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA, CHAIN! A; GT- BETA; CHAIN! B; GT-GAMMA; CHAIN! G;	GT-ALPHA/GF-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;
SEQFOL D score					119.11			
PMF	0.04	1.00	0.29	1.00			0.53	00:1
Verify	-0.06	0.57	0.40	0.38			0.14	0.64
Psi Blast	0.00032	4.8e-73	1.3e-58	1.6e-66	1.3e-77		1.3e-77	4.8e-54
END	352	431	285	373	370		328	431
STAR T AA	130	911	4	99	12		14	166
CHAI N ID	∢	¥	¥	∢	B		æ	В
PDB TD	lerz	Terj	lerj	lerj	1got		lgot	1got
SEQ NO:	1227	1227	1227	1227	1227		1227	1227

H 413 518 0.0068 -0.14 0.25 (GGCAPTE) CBAB 469.5.3 (GGCAPTE) CGCAPTE (GGC	FDB EDB	CHAI	STAR T AA	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation	
H 413 518 0.0068 -0.14 0.35 0.0022A) PAB, CEADR, A. B. L. H B 321 580 1.2e-15 -0.00 -0.18 0.002A) PAB, CEADR, A. B. L. H B 408 701 6.8e-16 0.11 -0.19 PAPD-LIES CHAPERONE PROC. CEANRS. A. C. E. G. I. K. M. G. HARIONE PROC. CEANRS. D. F. H. J. L. N. P. HARIONE PROC. CEANRS. D. F. H. J. L. N. P. HARIONE PROC. CEANRS. D. F. H. J. L. N. P. HARIONE PROC. CEANRS. A. C. E. G. I. K. M. G. CEANRS. G. G. I. K. M. G. CEANRS. G. G. I. K. M. G. CEANRS. G. G. G. I. K. M. G. CEANRS. G. G. G. I. K. M. G. CEANRS. G. G. G. I. K. M. G. CEANRS. D. F. H. J. L. N. P. HARIONE PROC. CEANRS. D. F. H. J. L. N. P. HARIONE PROC. CEANRS. D. F. H. J. L. N. P. HARIONE PROC. CEANRS. D. F. H. J. L. N. P. HARIONE PROC. CEANRS. D. F. H. J. L. N. P. HARIONE PROC. CEANRS. D. F. H. J. L. N. P. HARIONE PROC. CEANRS. E. P. CEANRS. E. PORA, CHAINS. A. B. PORA, CHAINS. G. B. C. CEANRS. E. PORA, CHAINS. G. B. P										BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	
413 518 0.00668 -0.14 0.35 0.0062A) FAB; CFBAB, A, B, B, L, B	-										
B 321 580 1.2e-15 -0.00 -0.18 PAPD-LIKEG CHAREOWICE-RING;	:=	æ	413	518	0.0068	-0.14	0.35		ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V REGION	
A 201 6.8e-16 0.11 0.19 PAPD-LINE CHANERONE FIMC, CHANGE, SECUPIC AND CHANGES, SECUPIC AND CHANGES,	E.	33	321	280	1.2e-15	-0.00	-0.18		PAPD-LIKE CHAPERONE FIMC;	CHAPERONE/STRUCTURAL	
B 408 701 6.8e-16 0.11 -0.19 PAPD-LINE CHAPERONE PIMC, CARNER, D. F. H. J. L. N. P.									MANNOSE-SPECIFIC ADHESIN	DONOR STRAND	
B 408 701 6.8e-16 0.11 -0.19									FIMH; CHAIN: B, D, F, H, J, L, N, P;	COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTTEN	
CHANN. A. C. G. J. K. M. O. A 214 203 0.00034 -0.25 0.13 SKP2, CHAIN: B. D. F. H. J. L. N. P. A 214 203 2.26-68 -0.22 0.38 PCRA, CHAIN: NULL; A 441 872 1.66-47 -0.55 0.00 AIT-DEPENDENT DNA HELICASE REP. CHAIN: A. B. PORA, CHAIN: C. P.	un	æ	408	701	6.8e-16	0.11	-0.19		PAPD-LIKE CHAPERONE FIMC:	CHAPERONE/STRUCTURAL.	
A 214 293 0,00034 -0.25 0,13 SRP2, CHAIN: A, E, F, H, J, L, N, CHAIN: B, D, F, H, J, L, N, CHAIN: B, D, CHAIN: A, D, CHAIN: CHAIN: A, CHAIN: C									CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN	PROTEIN CHAPERONE ADHESIN DONOR STRAND	
A 214 203 0.00034 -0.23 0.13 SKP2, CHAIN: A, C; SKP1; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: C, SKP1; CHAI									FIMH; CHAIN: B, D, F, H, J, L, N,	COMPLEMENTATION, 2	
A 214 293 0,00034 -0.25 0.13 SKP2; CHAIN: A, C; SKP1; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: C, SKP1; CHAIN: C, CHAIN: C, SKP1; CHAIN: C,									, ,	PROTEIN	
A 214 293 0,00034 -0.25 0.13 SKP2, CHAIN: A, C; SKP1; CFAIN: B, D; CFAIN:											
G0 960 3.2e.68 -0.22 0.58 PCRA, CIAIN: NULL;	23	∢	214	293	0.00034	-0.25	0.13		SKP2; CHAIN: A, C; SKP1; CHAIN: B. D;	LIGASE CYCLIN A/CDK2- ASSOCIATED P45: CYCLIN A/CDK2-	
430 960 3.2e-68 -0.22 0.58 PCRA, CHAIN NULL; A 441 872 1.6e-47 -0.55 0.00 HELCAS REP. FERP. FIAIN: A. B. PDRA CANN: C.										ASSOCIATED P19; SKP1, SKP2, F-	
430 960 3.2e-68 -0.22 0.58 PCRA, CITAIN NULL; A 441 872 1.6e-47 -0.55 0.00 ATP-DEPENDENT DNA HELICANS REP. CHAIN: A, B; DNA CALAN: C.										BOX, LRRS, LEUCINE-RICH	
490 960 5.2e-68 -0.22 0.58 PCRA, CHAIN: NULL; A 441 872 1.6e-47 -0.55 0.00 HELICANS REP. CHAIN: A. B. PDRA CHAIN: C. DNA CHAIN: C.										REPEATS, SCF, 2 UBIQUITIN, E3,	
A 441 872 1.66-47 -0.55 0.00 ATP-DEPENDENT DNA HELIOARE CHAIN: C. DNA CHAIN: C. DNA CHAIN: C. DNA CHAIN: C. DNA CHAIN: C.	١.,		430	0,00	3 20 68	0.00	0 20		DOBA, CHARLAIIII.	UBIQUILIN PROTEIN LIGASE	
A 441 872 1.66-47 -0.55 0.00 ATP-DEPENDENT DNA HELLCANE REP. CHAIN: A. B. DNA CHAIN: C. DNA CHAIN: C.	₹,		200	206	2.26-05	77.0-	0.38		PCKA; CHAIN: NULL;	HELICASE DNA REPAIR, DNA	
A 441 872 1.6e-47 -0.55 0.00 ATP-DEPENDENT DNA HELICASE REP, CHAIN: A, B; DNA CHAIN: C,										KEPLICATION, SOS KESPONSE,	
A 441 872 1.6c-47 -0.55 0.00 ATP-DEPENDENT DNA HELICASE REP. CHAIN: A. B. DNA CHAIN: C.										RINDING	
HELICASE REP. CHAIN: A, B; DNA CHAIN: C;	198	¥	441	872	1.6e-47	-0.55	0.00		ATP-DEPENDENT DNA	COMPLEX (HELICASE/DNA)	
DINA CHAIN: C;									HELICASE REP; CHAIN: A, B;	COMPLEX (HELICASE/DNA),	
4 40 70			,,,	T	0, 0,		Ī	,	DIVA CHAIN: C;	HELICASE, DNA UNWINDING	

	OENT CRA,	ASE), ASE 2 ASE 2	ASE) ASE 2 ASE 2 RICH	≼_	¥_	₹_	
tation	P-DEPENI	OR/NUCLE OR/NUCLE HYDROL SNITION, LEUCINE	COMPLEX (IN-HIBITOR/NUCLEASE) COMPLEX (RHIBITOR/NUCLEASE) COMPLEX (RH-ANG), HYDROLASEZ MOLECULAR RECOGNITION, BEPTOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP, RIBONUCLEOPROTEIN	R PLEX URNA), RN
PDB annotation	PCRA; A7 PCRA; HE SE, DNA,	(INHIBITY (INHIBITY (RI-ANG)) AR RECO (APPING,	(INHIBITY (INHIBITY (RL-ANG)) AR RECO	(NUCLEA NA) COM PROTEIN SONUCLE	(NUCLEA RNA) COM PROTEIN SONUCLE	(NUCLEA NA) COM PROTEIN SONUCLE	(NUCLEA RNA) COM PROTEIN
	HELICASE PCRA; ATP-DEPENDENT HELICASE PCRA; HELICASE PCRA; HYDROLASE, DNA, PRODUCT COMPLEX	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RL-ANG), HYDROLASE 2 MOI-ECULAR RECOGNITON, EPITOPE MAPPING, LEUCINE-RICH STREPATS	COMPLEX (IN-HIBITOR/NUCLEASE) COMPLEX (IN-HIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE Z MOLECULAR RECOGNITION, EBTTOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA SNRNP, RIBONUCLEOPRO	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA SNRNP, RIBONUCLEOPRO	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,
		1	, j.	oʻ	0	AIN: Q.	AIN: Q.
Coumpound	.A; CHAIN TP*TP*TI NA (5'-D(* DNA (5'- GP*C)-3');	NGIOGEN	NGIOGEN	IN IV; CH	IN IV; CH	IN IV; CH	INIV; CH
Cour	HELICASE PCRA; CHAIN: B, G; DNA (5'-D/*TP*TP*TP*TP*TJ-3'). CHAIN: C, D; DNA (5'-D(*GP*C)- 3'); CHAIN: H; DNA (5'- D(*AP*CP*TP*GP*C)-3'); CHAIN: I;	KIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	UZ RNA HARPIN IV; CHAIN: Q, R; UZ A'; CHAIN: A, C; UZ B"; CHAIN: B, D;	UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A'; CHAIN: A, C; UZ B"; CHAIN: B, D;	UZ RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A'; CHAIN: A, C; UZ B"; CHAIN: B, D;
	HELICASI DNA (5'-D CHAIN: C 3'); CHAIN D(*AP*CF CHAIN: 1;	CHAI	CHA	R; UZ CHAI	U2 R R; U2 CHAI	R; UZ CHA	R; UZ CHA
SEQFOL D score							
PMF		0.89	0.09	0.35	0.51	0.71	0.04
Verify		-0.01	0.04	0.04	0.28	0.36	0.04
Psi Blast		3.4c-22	6.4e-07	3.4e-13	3.2e-07	8.5e-24	3.4e-20
END		213	299	151	101	187	196
STAR		10	126	12	20	15	72
CHAI N ID		<	⋖	V	٧	4	¥
E G		la4y	la4y	1a9n	la9n	la9n	la9n
S E S		1237	1237	1237	1237	1237	1237

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PDB annotation	SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	CELL ÁDHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLITRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHONNE, ALPHA SUBUNIT, BETA SUBUNIT	TRANSFERASE CRYSTAL STRUCTURE, RAB ERRANYLITRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONNE, ALPHA SUBUNIT, BETA SUBUNIT	TRANSFERASE CRYSTAL STRUCTURE, RAB
Coumpound		UZ RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A'; CHAIN: A, C; UZ B"; CHAIN: B, D;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A:	INTERNALIN B; CHAIN: A;	RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D;	RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C, RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN:	RAB GERANYLOERANYLTRANSFE
SEQFOL D score									
PMF		0.35	9970	0.71	0.07	-0.02	0.96	0.94	-0.03
Verify		0.49	0.05	-0.14	-0.20	0.15	0.35	0.47	0.20
Psi Blast		3.20-07	5.10-24	3.2e-25	6.8e-29	6.4e-21	1.6e-11	3,2e-13	4.8e-10
END		101	192	187	221	268	100	233	278
STAR T AA		30	51	6	44	75	11	130	091
CHAI N ID		ပ	ပ	∢	¥	A	∢	∢	4
PDB CI		la9n	la9n	1406	9001	140b	Idce	Idee	ldce
SEQ B SEQ		1237	1237	1237	1237	1237	1237	1237	1237

PDB annotation		TRANSERASE CRYSTAL STRUCTURE, ANB GERANYLGERANYLTRANSFERASE, 2.0 A ZHRSOLUTION, N. FORAYTAMETHONINE, ALPHA SUBUNIT, BETA SUBUNIT	CONTRACTILE PROTEIN LEUCINE- RICH REPRAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEN, 2 CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	RNA BINDING PROTEIN TAP (NFX1); RBONUCLEOPROTEIN (RNP, RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2-
Coumpound	RASE ALPHA SUBUNIT; CHANN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN; B, D;	RAB GERANYLGERANYLTRANSFE ERASE ALPHA SUBUNIT; CHAIN: A, C, RAB GERANYLGERANYLTRANSFE GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D;	OUTER ARM DYNEIN; CHAIN: A;	OUTER ARM DYNEIN; CHAIN: A;	OUTER ARM DYNEIN; CHAIN: A;	NÚCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;
SEQFOL D score								
PMF		0.33	0.09	0.22	0.45	0.65	0.60	0.46
Verify		0.21	-0.31	-0.20	-0.54	-0.03	0.25	0.15
Psi Blast		3.2e-11	4.8e-12	3.2e-14	1.6e-11	1.1e-06	1.1e-06	1.2e-25
END		169	146	252	169	192	192	206
STAR T AA		4	=	130	37	132	132	10
CHAI		∢	∀	4	¥	<	В	٧
PDB		Idce	lds9	1ds9	1ds9	1foI	1601	1fs2
SEQ NO ID		1237	1237	1237	1237	1237	1237	1237

PDB annotation	ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE	LIGA'SE CYCLIN A/CDK2- ASSOCIATED P45, CYCLIN A/CDK2- ASSOCIATED P19, SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF2, DEMOUTHN, E3, BUJOUTHN PROTEIN LIGASE	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	HYDROLASE TETRATRICOPEPTIDE, TRE, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRF, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS,
PDB	ASSOCIATED P19; SKP1, SKP BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/ ASSOCIATED P19; SRP- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, PROTEIN LIGASE	ACETYLATION RNASE INH RIBONUCLEASE/ANGIOGER INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	HYDROLASE TETRATRICOPI TRP, HYDROLASE, PHOSPHA PROTEIN-PROTEIN INTERAC TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPI TRP, HYDROLASE, PHOSPHA PROTEIN-PROTEIN INTERAC TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPI TRP, HYDROLASE, PHOSPHA PROTEIN-PROTEIN INTERAC TPR, 2 SUPER-HELLX, X-RAY STRUCTURE	HYDROLASE TI TRP; HYDROLA PROTEIN-PROT
Coumpound		SKP2, CHAIN: A, C, SKP1, CHAIN: B, D;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 3; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;
SEQFOL D score							
PMF		0.22	0.82	0.80	0.51	0.76	0.23
Verify		0.34	-0.03	0.10	0.27	0.30	0.01
Psi Blast		1.16-06	1.5e-28	10-18	6.4c-14	4.8e-13	8e-13
END		294	223	279	250	296	153
STAR T AA		130	19	119	133	153	20
CHAI N ID		⋖					
EDB ED		1182	2bnh	la17	lal7	la17	1a17
Se o S		1237	1237	1238	1238	1238	1238

	T.		Γ.				
PDB annotation	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP: HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP: HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP: HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP: HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEFTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS.
Coumpound	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THRBONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THRBONING PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THRBONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;
SEQFOL D score						,	
PMF score	0.99	0.94	0.80	0.52	0.11	0.74	0.37
Verify score	0.31	0.56	0.22	0.22	0.18	-0.14	0.41
Psi Blast	5.1e-19	9.6e-13	9.6e-13	3.2e-14	1.7e-15	1.7e-18	4.8e-13
END	368	348	392	416	142	414	421
STAR T AA	221	232	263	290	29	300	338
CHAI N ID							
FDB CI	1a17	la17	la17	lal7	1a17	1a17	la17
SEQ NO:	1238	1238	1238	1238	1238	1238	1238

PDB annotation	IPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRE; HYDROLASE, PHOSFHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRF; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRY; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	TRANSFERASE FTASE; FTASE; FTASE, PTASE; FARNESYLTRANSFERASE; FARNESYL 2 TRANSFERASE, CAAX, RAS, CANCER	TRANSFERASE FTASE; FTASE, PET, PFTASE; FRNESYLTRANSFERASE; FARNESYL 2 TRANSFERASE; CAAX, RAS, CANCER
	TPR, 2 SUPER STRUCTURE	HYDROLASE TRP; HYDROI PROTEIN-PRO TPR, 2 SUPER STRUCTURE	HYDROLASE TRP; HYDROI PROTEIN-PRO TPR, 2 SUPER STRUCTURE	HYDROLASE TRP; HYDROJ PROTEIN-PRO TPR, 2 SUPER STRUCTURE	HYDROLASE TRP; HYDRO PROTEIN-PRO TPR, 2 SUPER STRUCTURE	TRANSFERASI FTASE, PFT, PI FARNESYLTR, FARNESYL 2 T RAS, CANCER	TRANSFERASI FTASE, PFT, PF FARNESYLTR, FARNESYL 2 FARNESYL 2 RAS, CANCER
Coumpound		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THRBONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	FARNESYLTRANSFERASE (ALPHA SUBNUTI); CHAIN: A; FARNESYLTRANSFERASE (BETA SUBUNIT); CHAIN: B; K- RASHS PEPTIDE SUBSTRATE; CHAIN: P;	FARNESYLTRANSFERASE (ALPHA SUBUNIT); CHAIN: A; FARNESYLTRANSFERASE (BETA SUBUNIT); CHAIN: B; K- RASAB PEPTIDE SUBSTRATE;
SEQFOL D score							
PMF score		0.70	0.41	0.58	0.65	0.60	0.18
Verify		0.18	0.34	0.12	0.12	-0.23	-0.04
END Psi Blast AA		1.70-15	8e-10	4.8e-11	3.4e-17	4.8e-07	3.4e-15
		184	175	509	212	410	266
STAR		99	63	85	68	217	28
CHAI						∀	٧
PDB		la17	la17	la17	1a17	148d	148d
SEQ UD NO:		1238	1238	1238	1238	1238	1238

PDB annotation	SIGNALLING COMPLEX RACI; POTPHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF	SIGNALLING COMPLEX RACI; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF	SIGNALLING COMPLEX RACI; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTTE	SIGNALLING COMPLEX RACI; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF	SIGNALLING COMPLEX RACI; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTTE	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN,
Coumpound	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NGF-2) CHAIN: B;	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CITAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE I; CIAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPRZA-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP;
SEQFOL D score								
PMF	0.48	0.76	86.0	0.86	0.21	0.47	1.00	96'0
Verify score	0.15	0.40	0.14	0.05	0.12	0.38	0.24	0.02
Psi Blast	1.4e-09	8c-10	4.8e-09	4.8e-09	0.00016	6.4e-15	6.4e-15	1.6e-10
END	278	322	379	417	244	247	252	283
STAR	135	189	229	290	29	133	191	195
CHAI N ID	В	В	м	В	Д	∢	¥	A
PDB	1696	9691	1e96	1e96	1e96	lelr	lelr	lelr
SEQ ID NO:	1238	1238	1238	1238	1238	1238	1238	1238

	_			_	_	_						_	٦			Т				_		_	-	_	_
PDB annotation	PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN	BINDING	CHAPERONE HOP, TPR-DOMAIN,	PEPTIDE-COMPLEX, HELICAL REPEAT HSP90 2 PROTEIN	BINDING	CHAPERONE HOP, TPR-DOMAIN,	PEPTIDE-COMPLEX, HELICAL	REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN,	PEPTIDE-COMPLEX, HELICAL	REPEAT, HSP90, 2 PROTEIN	BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX. HELICAL	REPEAT, HSP90, 2 PROTEIN	DINDING	CHAPERONE HOP, TPR-DOMAIN,	PER LIDE-COMPLEA, HELICAL	BINDING	CHAPERONE HOP, TPR-DOMAIN,	PEPTIDE-COMPLEX, HELICAL	REPEAT, HSC70, 2 HSP70, PROTEIN	BINDING	CHAPERONE HOP, TPR-DOMÁIN, BEBTINE COMBIEV HEI IGAI	REPEAT, HSC70, 2 HSP70, PROTEIN
Coumpound	CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD: CHAIN: B:		TPR2A-DOMAIN OF HOP;	MEEVD: CHAIN: B:	, , , , , , , , , , , , , , , , , , , ,	TPR2A-DOMAIN OF HOP;	CHAIN: A; HSP90-PEPTIDE	MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP;	CHAIN: A; HSP90-PEPTIDE	MEEVD; CHAIN: B;		TPR2A-DOMAIN OF HOP; CHAIN: A: HSP90-PEPTIDE	MEEVD; CHAIN: B;	THE REAL PROPERTY OF THE PARTY	IPRI-DOMAIN OF HOP CHAIN:	A, b; nsc/0-rer libe; chain:	ž,	TPR1-DOMAIN OF HOP; CHAIN:	A, B; HSC70-PEPTIDE; CHAIN:	C, D;		TPRI-DOMAIN OF HOP; CHAIN:	C, D;
SEQFOL D score																									
PMF		66.0		0.74			0.29			0.55				0.33		8	0.99			96.0				1.00	
Verify score		0.47		0.27			0.13			0.54				0.31		27.0	0.40			0.47				0.63	
Psi Blast		4.8e-12		3.2e-13			4.8c-11			4.8e-12				1.16-11			1.16-13			1.3e-12				3.2e-10	
END		326		355			117			419				185			177			292				296	
STAR T AA		228		262			28			334				83		2	5			153				196	
CHAI		¥		¥			Ą			A				¥			<			<				¥	
ED GI		leir		leir			1elr			lelr				leir		1-1-1	ie!w			lelw				lelw	
SEQ No de		1238		1238			1238			1238				1238		1000	1738			1238				1238	

PDB annotation		CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTSI- BR. PEROXIN-S, PTSI PROTEIN. PEPTIDE COMPLEX, TETRARIRCOPETIDE REPEAT, TPR, 2 HELICAL REPEAT	SIGNALING PROTEIN PEROXISMORE DECEPTOR 1 DTS1
PDB	BINDING	CHAPERONE HO PEPTIDE-COMP REPEAT, HSC70 BINDING	CHAPERONE HO PEPTIDE-COMP REPEAT, HSC70 BINDING	CHAPERONE HO PEPTIDE-COMP REPEAT, HSC70 BINDING	CHAPERONE HO PEPTIDE-COMP REPEAT, HSC70 BINDING	CHAPERONE HO PEPTIDE-COMP REPEAT, HSC70 BINDING	CHAPERONE HO PEPTIDE-COMP REPEAT, HSC70 BINDING	SIGNALING PROTEIN PEROXISMORE RECEI BP. PEROXIN-5, PTS1 1 PEPTIDE COMPLEX, TETRATINICOPEPTIDE 2 HELICAL REPEAT	SIGNALING PROTEIN PEROXISMORE RECE
Coumpound		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL I RECEPTOR, CHAIN: A, B; PI'SI-CONTAINING PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR: CHAIN:
SEQFOL D score									
PMF		00:1	0.57	0.03	0.98	0.21	0.82	00.1	96.0
Verify score		0.76	0.32	0.25	0.23	0.29	0.32	0.32	0.07
Psi Blast		4.8e-13	4.8e-10	6.4e-14	3.2e-15	1.16-11	6.4e-10	9.66-38	3.2e-09
END		332	122	86	408	419	155	413	420
STAR		236	25	2	304	342	19	166	313
CHAI N ID		Ą	4	V V	<	∢	V	A	A
PDB		lelw	le]w	lelw	lelw	leíw	lelw	1feh	1fch
SEQ No ID		1238	1238	1238	1238	1238	1238	1238	1238

PDB annotation	PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRARICOPETIDE REPEAT, TPR, 2 HELICAL REPEAT	SIGNALINO PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PETTIDE COMPLEX, FETTAR TRICOPETTIDE REPEAT, TPR, 2 HELICAL REPEAT	SIGNALIMO PROTEIN PEROXISMORE RECEPTOR I, PTSI- BP, PEROXIN-S, PTSI PROTEIN- BP, PEROXIN-S, TTSI PROTEIN- BETTIDE COMPLEX, TETRATRUCOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS I AND 2, ECADI2; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS I AND, ECADDIS, CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1
Coumpound	PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: A, B, PTSI-CONTAINING PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: A, B; PTSI-CONTAINING PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: A, B; PTSI-CONTAINING PEPTIDE; CHAIN; C, D;	B-CADHERIN; CHAIN: A, B;	E-CADHERIN; CHAIN: A, B;	E-CADHERIN; CHAIN: A, B;
SEQFOL D score							
PMF		1.00	1.00	1.00	0.55	97.0	0.64
Verify		0.48	0.38	0.46	0.10	-0.19	0.21
Psi Blast		6.4e-31	1.3e-29	4.8e-29	3.2e-20	6.8e-27	4.8e-17
END		273	220	345	152	253	255
STAR T AA		34	7	86	34	25	83
CHAI N ID		∢	⋖	¥	A	∢	V
FDB ID		1fch	lfgh	Ifch	ledh	ledh	ledh
SEQ NO:		1238	1238	1238	1241	1241	1241

PDB annotation	AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN	CELL ADHESION PROTEIN CADHERIN INCI 13	CELL ADHESION PROTEIN CADHERIN INCI 13	CELL ADHESION PROTEIN CELL ADHESION PROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN	METAL BINDING PROTEIN BETA SANDWICH, CALCIUM-BINDING PROTEIN, METAL BINDING 2 PROTEIN	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPFAT	ANTI-ONCOGENE CELL CYCLE,
Coumpound		N-CADHERIN; INCI 3	N-CADHERIN; INCI 3	N-CADHERIN; CHAIN: A;	N-CADHERIN; CHAIN: A;	N-CADHERIN; CHAIN: A;	LAMININ ALPHA2 CHAIN; CHAIN: A, B, C, D;	EPITHELIAL CADHERIN; CHAIN: NULL;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	TUMOR SUPPRESSOR P16fNK4A; CHAIN: NULL;	TUMOR SUPPRESSOR PIGNK4A; CHAIN: NULL;	TUMOR SUPPRESSOR
SEQFOL D score													66.97
PMF		0.04	0.31	0.28	0.65	0.35	0.40	0.04	1.00	1.00	1.00	0.93	
Verify score		-0.07	0.15	-0.20	-0.03	-0.20	-0.08	-0.22	0.56	0.40	0.84	0.39	
Psi Blast		5.1e-06	1.7e-05	1.4e-21	1.7e-21	6.4c-17	3.4e-20	1.7e-07	3.4e-30	3.4e-30	5.1e-29	1.5e-29	3.4e-30
END		253	152	152	253	255	549	154	262	330	359	385	393
STAR T AA		206	56	34	43	06	358	43	132	991	202	233	233
CHAI N ID		В	В	A	A	A	∢						
FDB ID		Inci	Inci	lncj	Incj	Incj	1qu0	lsuh	la5e	la5e	la5e	la5e	laSe
SEQ No. 10		1241	1241	1241	1241	1241	1241	1241	1246	1246	1246	1246	1246

PDB annotation	ANTI-ONCOGENE, REPEAT, ANK REPEAT	COMPLEX (TRANSCRIPTION REGULATIONIDNA) GABPALPHA; GABRBETA I; COMPLEX (TRANSCRIPTION TREGULATIONIDNA), DNA-BINDING, 2 NUCLEAR PROPER), ETS DOMAIN,	ATS, 43 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA;	MPLEX	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN.	ATS,	VSCRIPTION	REGULATION/DNA) GABPALPHA;	MPLEX	(IRANSCALFILON REGIL ATTOMONA) DNA-BINDING	2 NUCLEAR PROTEIN, ETS DOMAIN,	ATS,	43 FACTOR	COMPLEX (TRANSCRIPTION PEGIT ATTOMENA) GABBAI BHA:	MPLEX	z	REGULATION/DNA), DNA-BINDING,	NUCLEAR PROTEIN, ELS DOMAIN,	/
PDB	ANTI-ONCOGEN REPEAT	COMPLEX (TRANSCRIPTION REQULATIONDNA) GABPAL GABPETAI; COMPLEX (TRANSCRIPTION REGULATIONDNA), DNA-BI	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPAI	GABPBETA1; COMPLEX (TRANSCRIPTION	2 NUCLEAR PRO	ANKYRIN REPEATS,	COMPLEX (TRANSCRIPTION	REGULATION	GABPBETA1; COMPLEX	PEGII ATTONIO	2 NUCLEAR PRO	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	GABPBETA1: COMPLEX	(TRANSCRIPTION	REGULATION/D	Z NUCLEAR PRO	A L K L K L K L K L K L K L K L K L K L
Coumpound	PIGINK4A; CHAIN: NULL;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, B;		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	PROTEIN BETA I; CHAIN: B; DNA: CHAIN: D. E:			GA BINDING PROTEIN AT PHA-	CHAIN: A, GA BINDING	PROTEIN BETA I; CHAIN: B;	DINA, CHAIN. D, B,			the state of the s	GA BINDING FROTEIN ALPHA;	PROTEIN BETA 1: CHAIN: B:	DNA; CHAIN: D, E;			
SEQFOL D score																				
PMF		00.1		I.00				100	3					9	3					
Verify		50:1		0.93				0.07	3					8	0.93					
Psi Blast		le-43		le-39				9 60-41						1 6. 20	1.0e-58	_				_
END		298		165				208	}					371	6					_
STAR		145		14				150	3					ţ	=					
CHAI N ID		я		В				4	1					0	n					
PDB		lawc		lawc				lawc	2					James 1	lawc					
SEQ NO:		1246		1246				1246	?					10.45	0571					_

PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPH4; GARPBETAL; COMPLEX (TRANSCRIPTION REGULA TION/DNA), DIAM-BINDING REGULA TION/DNA), DIAM-BINDING 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEAT,	COMPLEX (TRANSCAPTION REGULATION/DNA) GARPHETH; GARPHETH; COMPLEX (TRANSCRETION TRANSCRETION 2 NUCLEAR PROTEIN, ETS DOMAIN, ANX TRANSCRETION 3 FACTOR	COMPLEX (TRANSCRPTION REGULATIONDNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRPTION EGGLATIONDNA), DAN-BINDING, EGGLATIONDNA, DAN-BINDING, 2 NUCLEAR PROTEM, ETS DOMAIN, ANKYRIN REPEAT, KRANSCRPTION 3 PACTOR		-
Coumpound	da Binding protein alpha; Chani: a; da Binding Protein Beta i; chain: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CARINI: A; GB BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHARIN: 4; GB BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GB BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING
SEQFOL D score				90.97	
PMF	0.00	1.00	0:00		0.23
Verify	0.84	0.55	0.77		0.21
Psi Blast	3.4e-39	9.6e-35	le-40	le-43	3.2e-32
END	332	332	362	363	395
STAR T AA	183	184	212	212	217
CHAI N 1D	щ	д	æ	д	В
PDB ID	lawc	lawc	lawc	lawc	lawc
SEQ NO:	1246	1246	1246	1246	1246

und PDB annotation	CHAIN: B; (GABPBETAI; COMPLEX (TRANGRIPTION) ENGULATIONDNA), DIA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKTRIN REPEATS, TRANSCRIPTION 3 FACTOR	TEIN ALPHA; COMPLEX (TRANSCREPTON) DING CHAIN: B; CARABETAL; COMPLEX CHAIN: B; CARABETAL; COMPLEX (TAANSCREPTON REGILATIONADA, DIAM-SENDING, 2 NUCLEAR REOTEM, ETS DOMAIN ANYKRIN REBERTA; ETS DOMAIN TRANSCRIPTON 3 FACTOR	TIEN ALPHA; COMPLEX (TRANSCREPTON) DING CHAIN: B; GARBETALI; COMPLEX CHAIN: B; CARASCREPTON REGULATIONOMA, DIA-BIRDING, REGULATIONOMA, DIA-BIRDING, 2 NUCLEAR REOTEN TRANSCREPTON 3 FACTOR			t
Coumpound	PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BRUDNG PROTBIN ALPHA; CARAN: A; GB BRUDNG PROTBIN BETA I; CHAIN! B; DNA; CHAIN! D, E;	GA BINDING PROTEIN ALPHA; CARANE, 4, GAB BINDNG PROTEIN BETA 1; CHAINE B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAINE, AG BBINDING PROTEIN BETA 1; CHAIN! B; DNA; CHAIN: D, E;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	The same and the same of the same of
SEQFOL D score					87.65	
PMF		00.1	00.1	1.00		00.
Verify score		0.88	0.55	9.68		000
Psi Blast		1.6e-33	8.5e-39	9.6e-37	8e-30	0.00
END AA		132	199	199	301	301
STAR T AA		m	45	20	145	153
CHAI		ш	щ	m		
PDB OI		lawc	lawc	lawc	8P91	1148
SEQ No. 10		1246	1246	1246	1246	1246

PDB annotation	SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	COMPLEX (KINASE/ANTI- ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT	KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN,	CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (PRIASPANT)	ONCOGENE) HEADER	COMPLEX (INHIBITOR	PROTEINKINASE) INHIBITOR PROTEIN CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	COMPLEY (NITIBILION	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR DEOTERN/CENASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX
Commpound	CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN:	ú			CYCLIN-DEPENDENT KINASE	6; CHAIN: A; FISINK4D; CHAIN: R:	î			CYCLIN-DEPENDENT KINASE 6: CHAIN: A: P19INK4D: CHAIN:	B.			CVCI IN DEBENDENT VINASE	6; CHAIN: A; P19JNK4D; CHAIN:	B;			TO 11 COM THE COURT OF THE PARTY OF THE PART	CYCLIN-DEPENDENT KINASE	B:	•
SEQFOL D score															78 04								
PMF		1.00				0.10					00.1									200	1.00		
Verify score		0.57				0.10				000	0.93									0 40	0.73		
Psi Blast		1.7e-28				3.4e-38					1.76-39				6.88-40					0.4.0	3.4e-38		
END		365				304				000	0/1				303	}				900	338		
STAR T AA		244				114				,	2				147						183		
CHAI		В				В				,	n				2					-	n		
PDB		Tbi7				Iblx					IDIX				J.P.					1	XIQI		
SEQ No.		1246				1246				27.07	1240				1246	!				27.01	0471		

PDB annotation	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR		KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX		PROTEIN/KINASE) INHIBITOR		ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR			 ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	P18NK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE,	HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	P18INIK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE,	HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE,	I I OUND IN THE COLOR
Coumpound		CYCLIN-DEPENDENT KINASE 6: CHAIN: A: P19INK4D: CHAIN:	B;			CYCLIN-DEPENDENT KINASE	6; CHAIN: A; PI9INK4D; CHAIN: B.	á.			CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	B			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;				CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;				CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;			
SEQFOL D score																														_
PMF		1.00				9.1					1.00					1.00					1.00					1.00				
Verify		68'0				0.70					1.03					82.0					0.97					0.87				
Psi Blast		1.7e-38				1.5e-38					6.8e-40					6.8e-37					1.6e-36					9.6e-37				
END AA		368				205					237					310					303					170				
STAR T AA		215				20					82					144					150					12				
CHAI N ID		В				Д					В					Ą					٧					٧				
EDB EDB		16lx				Iblx					1blx					lbu9					1bu9					1bu9				
SEQ NO:		1246				1246					1246					1246					1246					1246				

PDB annotation	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- TONGC, CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INVAC; CELL CYCLE INHIBITOR, P18INKAC; TUMOR, SUPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INVAC; CELL CYCLE INHIBITOR, P18INKAC; TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- NKAC; CELL CYCLE INHIBITOR, P18INKAC; TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR, SUPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INFIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE.
Coumpound	CYCLIN-DEPENDENT KINASE 6 INHIBITOR, CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR, CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR, CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;
SEQFOL D score							89.81
PMF	00.1	66.0	0.1	00.1	0.51	0.1	
Verify	0.61	0.25	0.63	0.79	0.47	0.94	
Psi Blast	le-35	8e-33	3.4e-35	6.8e-33	3.4c-37	1.7e-39	1.7e-39
END	338	367	373	394	174	205	117
STAR T AA	181	184	215	243	К	44	6
CHAI N ID	A	4	٧	4	٧	∀	A
PDB ID	PudI	6ng1	lbu9	1bu9	1bu9	1bu9	lbu9
SEQ NO:	1246	1246	1246	1246	1246	1246	1246

PDB CHAI STAR									
PDB CHA STAR END Psi Blast Verity Phf; Store Discretion	PDB annotation	HORMONE/GROWTH FACTOR CELL CYCLE INHIBITOR P18- INK-4C(INK.6); CELL CYCLE INHIBITOR, P18-INK-4C(INK.6), ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR PIS- CELL CYCLE INHIBITOR PIS- INKAC(INKG), CELL CYCLE INHIBITOR, PIS-INKAC(INKG), NAKYRIN REPEATI, 2 CDK 4/6 INHIBITOR	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN KEPEAT; 2 CDK 4/6 INHIBITOR	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INFIBITOR, P18-INK4C(INK6), ANYYRIN REPEAT, 2 CDK 4/6 INTIRITOR	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65;
PDB CHA STAR END Phi Blast Verify PMF	Coumpound	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA: CHAIN: D:	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; 1-KAPPA- B-AI PHA: CHAIN: D;	NF-KAPPA-B PG5 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA: CHAIN: D:	SUNIT;
PDB CHAI STAR END Psi Blast Verify	SEQFOL D score				83.68				
Pub CHA STAR EAD Psi Blast	PMF	1.00	1.00	00:1		1.00	0.92	0.35	1.00
PDB CHAI STAR END D NID TAA AA	Verify	0.88	0.78	0.28		0.47	0.20	0.22	0.18
PDB CHAI STAR D		6.4e-36	3.2e-36	3.2e-32	3.2e-36	4.8e-35	1.6e-30	1.6e-34	8e-43
PDB CHAI D N	END	302	169	366	236	186	346	404	232
In D	STAR	150	17	184	81	12	179	212	45
PDB IIIIb IIIIb IIIIb IIIIb IIIIb IIIIb IIIIb IIIIb IIIIb IIIIIb IIII	CHAI N ID	V	4	-	₹.	Ω	А	Д	Д
	PDB	lihb	lihb	qiil	Lilb	Lika	iika	lika	1ikn
	SEQ NO:	1246	1246	1246	1246	1246	1246	1246	1246

PDB annotation	PSOD; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65, P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	COMPLEX (TRANSCRIPTION REGANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REGANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYKIN 2 REPEAT HELLX	COMPLEX (TRANSCUPTION REGANK REPEAT) COMPLEX (TRANSCUPTION REGULATIONANK REPEAT), ANKYRN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REGIANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRN 2 REPEAT HEI JX	COMPLEX (TRANSCRIPTION REGIANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYKIN 2 REPEAT HELLX
Coumpound	CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	MYOTROPHIN; CHAIN: NULL	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NP-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; HKAPPA-B-ALPHA; CHAIN: B, F;	NP-KAPPA-B P65; CHAIN: A, C; NP-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; J-KAPPA-B-ALPHA; CHAIN: E, F;
SEQFOL D score		80.97	68.11					
PMF				1.00	1.00	1.00	1.00	1.00
Verify				0.69	0.81	0.55	0.62	0.65
Psi Blast		8e-43	9.6e-25	1.7e-48	1.4e-35	5.1e-47	1.7e-48	4.8e-30
END		253	130	311	186	338	367	346
STAR		45	12	113	11	143	177	178
CHAI N ID		Q		ш	щ	ы	п	ш
FDB ED		lika	lmyo	9	lnfi	Infi	Infi	ja i
SEQ No in		1246	1246	1246	1246	1246	1246	1246

PDB annotation	COMPLEX (TRANSCRIPTION REGGANK REPEAT) COMPLEX (TRANSCRIPTION REGULATIONANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REGIANK REPEAT) COMPLEX (TRANSCRIPTION REGULATIONANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REGIANK REPEAT) COMPLEX (TRANSCRIPTION REGULATIONANK REPEAT), ANKYRIN 2 REPEAT HELLX	COMPLEX (TRANSCRIPTION REGANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRPTION REGULATION/ANK REPEAT), ANKYRN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRPTION REGULATION/ANK REPEAT), ANKYRN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REGANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT),
Coumpound	NP-KAPPA-B P65; CHAIN: A, C; NP-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NP-KAPPA-B P65; CHAIN: A, C; NP-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: B, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CIAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; F; F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;
SEQFOL D score					89.07		
PMF	1.00	0.21	1.00	1.00		1.00	1:00
Verify score	0.85	0.26	0.53	0.53		0.74	0.66
Psi Blast	3.4e-38	9.6c-35	1.5e-44	1.7e-51	1.7e-51	1.6e-42	5.1e-50
END	170	404	394	238	242	232	278
STAR T AA	17	210	215	43	43	44	82
CHAI N ID	ш	ш	н	ш	ш	ш	ш
FDB DD	Inf	ja ja	lni	Ħ	gu]	Jul	Infi
SEQ ID NO:	1246	1246	1246	1246	1246	1246	1246

	_							
PDB annotation	ANKYRIN 2 REPEAT HELIX	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE	ONCOGENEZA (ANT.) ONCOGENEZA (ANT.) ONCOGENEZA (ANT.) STRAPEZA (ANT.) MULTIGENE Z PANDLY, NUCLEAR NUTTIGENE Z PANDLY, NUCLEAR DISSASSE MULTITON, DISSASSE MULTITON, ONCOGENEZANCY (ANT.) ONCOGENEZANCY ONCOGENEZANCY ONCOGENEZANCY ONCOGENEZANCY ONCOGENEZANCY ONCOGENEZANCY ONCOGENEZANCY		STRUCTURAL PROTEIN TWO REPEATS OF SPECTEIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COLLED-COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	GROWTH FACTOR NEU DIFFERENTIATION FACTOR (RAT), ACETYLCHOLINE GROWTH FACTOR	
Coumpound		REGULATORY PROTEIN SWI6; CHAIN: A, B;	P53; CHAIN: 4; 53BP2; CHAIN: B;		ALPHA SPECTRIN; CHAIN: A, B, C;	ALPHA SPECTRIN; CHAIN: A, B, C;	HERBÜLIN-ALPHA; CHAIN: NULL;	GROWTH FACTOR HEREGULIN-ALPHA (EPIDERAAL GROWTH FACTOR-LIKE DOMAIN) 1HRE 3 (NMR, AINIMIZEDA AVERAGE STRUCTURE) 1HRE 4
SEQFOL D score		60.99	69.71					
PMF					0.29	0.03	0.11	0.25
Verify					-0.03	0.02	0.07	0.13
Psi Blast		1.36-21	3.2e-18		5.1e-12	5.1e-07	0.0051	0.0051
END AA		320	398		591	651	150	150
STAR T AA		76	214	_	375	436	120	120
CHAI N ID		¥	В		∢			
FDB TD		1sw6	1ycs		lcun	lcun	Ihae	lhre
SEQ ID NO:		1246	1246		1250	1250	1250	1250

PDB annotation	APOPTOSIS TRAIL; DR5; LIGAND- RECEPTOR COMPLEX, TRIMERIC JELLY-ROLL, TNF-R 2	SUPERFAMILY, APOPTOSIS BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-ACTON, STREGEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	SERNUT PROTEINASTE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODIJLN, IVA, CD141 ANTIGENE, EGR-CAKK SERNE PROTEINASE, EGF-LIKE DOMAINS, ANTIGEOGGULANT COMPLEX, ANTIGEOGGULANT COMPLEX, ANTIGENENO, THE COMPLEX	SERURE PROTEINASE COAGULATION FACTOR II; FETOMODULA, INA, CD14 ANTICER, EGG-CAK SERURE PROTEINASE, EGF-LIKE DOMAINS, ANTICOGGULAAT COMPLEX, 2 ANTICOGGULAAT COMPLEX, 2	SERUNE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; ETOMOGULATION PACTOR II FTOMOGULATION FACTOR II ANTIGEN; EGR-COM SERINE PROTEINASE, EGF-LICE DOMAINS, ANTICOAGIT ANTI COMPIEX 9
Coumpound	TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: B; DEATH RECEPTOR 5; CHAIN:	A; BLOOD COAGULATION BLOOD COAGULATION FACTOR VIIA; CHAIN: I, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U, D-PHE-PIES-ARG- CHLOROMETHYLKETONE OFFROMETHYLKETONE	THROMBIN LIGHT CHAIN; HEATY CHAIN, CHAIN, CHAIN, M. N. PRAY CHAIN, CHAIN, M. N. CHAIN, I, S. I, THROMBIN DIHIBITOR L-GLU-L-CLY-L ARM, CHAIN: B, F, G, H;	THROMBIN LIGHT CHAIN: CHAIN: A, B, C, D; THROMBIN HEAYY CHAIN: CHAIN: M, N, CHAIN: I, X, L; THROMBIN CHAIN: I, X, L; THROMBIN NHIBITOR LGLUL-GCY-L- ARM; CHAIN: E, F, G, H;	THROMBIN LIGHT CHAIN; CHANN, A. B., C. B. THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P. THROMBOMODULIN; CHAIN: I. J. K., THROMBIN INHBITOR L-GLU-L-GLY-L-
SEQFOL D score			-		
PMF	-0.14	-0.13	-0.20	-0.20	-0.19
Verify score	0.10	0.06	0.02	0.03	07.0
Psi Blast	5.1e-10	8c-09	3.2e-12	6.4e-15	1.1e-12
END AA	426	449	346	394	436
STAR T AA	326	351	233	268	308
CHAI N ID	4	ı		_	H
EDB EDB	1d4v	1dan	1dx5	1dx5	1dx5
SEQ No ib	1252	1252	1252	1252	1252

PDB annotation	ANTIFIBRINOL YTIC COMPLEX	MATRIX PROTEIN	EXTRACELLULAR MATRIX,	CALCIUM-BINDING,	GLYCOPROTEIN, 2 REPEAT,	SIGNAL, MULTIGENE FAMILY,	DISEASE MUTATION, 3 EGF-LIKE	DOMAIN, HUMAN FIBRILLIN-1	FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN	EXTRACELLULAR MATRIX.	CALCIUM-BINDING,	GLYCOPROTEIN, 2 REPEAT.	SIGNAL, MULTIGENE PAMILY.	DISEASE MUTATION 3 EGE-LIKE	DOMAIN, HUMAN FIBRILLIN-1	FRAGMENT, MATRIX PROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	COMPLEX (BLOOD	COAGULATION/INHIBITOR)	CHRISTMAS FACTOR; COMPLEX,	INHIBITOR, HEMOPHILIA/EGF,	BLOOD COAGULATION, 2 PLASMA,	SERINE PROTEASE, CALCIUM-	BINDING, HYDROLASE, 3	GLYCOPROTEIN	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INTIBLIOR, 2 SERING PROTEASE
Coumpound		FIBRILLIN; CHAIN: NULL;								FIBRILLIN; CHAIN: NULL;								LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN; NULL;	LAMININ; CHAIN: NULL;	FACTOR IXA; CHAIN: C, L,; D-	PHE-PRO-ARG; CHAIN: I;							ANTISTASIN; CHAIN: NULL;				
SEQFOL D score																			132.10															
PMF		0.04								-0.19								0.93		0.51	-0.03	-0.17								-0.14				
Verify		0.24								80.0								0.17		0.40	-0.00	0.10								0.34				
Psi Blast		1.6e-13								3.2e-10								8.5e-39	8.5e-39	1.6e-20	3.2e-18	3.2e-09								3.4e-17				
END		395								431								614	411	452	496	441								414				
STAR T AA		307								351								225	234	293	358	351								319				
CHAI N ID																						T												
PDB ID		lemn								lemn								Iklo	1klo	1klo	1klo	1pfx								Iskz				
SEQ No: D		1252								1252								1252		1252	1252	1252								1252				

PDB annotation	INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR;	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	DI DOD COACIII ATTONI BACTOR	STUART FACTOR; BLOOD	COAGULATION FACTOR, SERINE	GROWTH FACTOR LIKE DOMAIN					LYASE 2-PHOSPHO-D-GLYCERATE HYDROLASE; LYASE, GLYCOLYSIS	LYASE (CARBON-OXYGEN) 2-	PHOSPHO-D-GLYCERATE DEHYDRATASE: 1PDZ 6	PROTEIN KINASE INHIBITOR PKCI-	1, PROTEIN KINASE C INHIBITOR 1,	PKCI-1. HIT PROTEIN FAMILY. 2	HISTIDINE TRIAD PROTEIN	FAMILY, NUCLEOTIDYL	HYDROLASE, 3 NUCLEOTIDYL TP ANSTER A ST	PROTEIN KINASE INHIBITOR PKCI-
Coumpound		ANTISTASIN; CHAIN: NULL;			PLOOD COACIII ATION	FACTOR XA; CHAIN: L, C;			METALLOTHIONEIN	METALLOTHIONEIN ISOFORM II 4MT2 3	LECTIN (AGGLUTININ) WHEAT	(ISOLECTIN 2) 9WGA 3	ENOLASE; CHAIN: A, B;	ENOLASE; 1PDZ 4 CHAIN:	NULL; IPDZ 5	PROTEIN KINASE C	INTERACTING PROTEIN;	CIOIL NOTES				PROTEIN KINASE C
SEQFOL D score																						144.01
PMF		0.19			010	-			0.00		-0.19		1.00	1.00		1.00						
Verify		0.16			0.14				-0.05		0.04		0.25	0.15		96.0						
Psi Blast		5.1e-10			2 20 00				1.3e-09		4.8e-15		9.6e-61	8e-63		9.6e-41						9.6e-41
END		425			440	?			428		492		134	137		163						163
STAR		355			255	3			368		298		=	==		53						53
CHAI N 1D					L						¥		¥									
FDB ID		1skz			1.60				4mt2		9wga		lone	lpdz		Ikpf						Ikpf
SEQ ID NO:		1252			1252	!		Ī	1252		1252		1253	1253		1256						1256

PDB annotation	I, PROTEIN KINASE C INHIBITOR I, HINT PROTEIN KINASE NHBITOR, PRCCI, HIT PROTEIN FAMILY, 2 HSTIDINE TRAD PROTEIN PAMILY, X INCLEOTIDY, HYDROLASE, S NUCLEOTIDYL HYDROLASE, S NUCLEOTIDYL	NUCLEOTIDE-BINDING PROTEIN HINT; NUCLEOTIDE-BINDING PROTEIN	NUCLEOTIDE-BINDING PROTEIN HINT; NUCLEOTIDE-BINDING PROTEIN	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	COMPLEX (TRANSCRIPTION REGULATION/DNA) GARPALPHA; GABBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING REGULATION/DNA), DNA-BINDING NUCLEAR PROTEIN, ETS DOMAIN, ANKTRIN REPEAT, TRANSCRIPTION 3 FACTOR
Coumpound	INTERACTING PROTEIN; CHAIN: NULL;	HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN; CHAIN: NULL;	HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN, CHAIN: NULL;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	GA BINDING PROTEIN ALPHA; CARN: A; GB BINDING PROTEIN B; B; GARN: B; DNA; CHAIN: D, B;
SEQFOL D score		147.29						
PMF			1.00	0.48	1.00	00:1	0.40	1.00
Verify			0.86	0.27	0.80	0.65	0.16	19:0
Psi Blast		6.4e-41	6.4e-41	1.4c-21	8e-26	3.4e-25	4.8e-18	6.4e-37
END		163	163	151	154	162	121	164
STAR T AA		47	52	39	39	19	9	39
CHAI N ID								В
PDB CI		4rhn	4rhn	la5e	1a5e	1a5c	lase	lawc
SEQ Signal Signa		1256	1256	1257	1257	1257	1257	1257

PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GARBETAI, COMPLEX (TRANSCRIPTION TRANSCRIPTION 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKTRIN REPEATS.) TRANSCRIPTION 3 PACTOR	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	ONCHEZ KONZBEATT ONCOGENE) CDKGE PIGNKGAA KNASE, CYCLIA DEBENDENT KNASE, CYCLIA DEBENDENT KNASE NHEBITONY 2 PROTEIN CONCENE, NRA, CELL CYCLE, MOLTIFUE TUMOR SUPRESSOR, 3 MITSI, ONCOGENE) FRADER ONCOGENE) FRADER	ONOCIETE (CIVESTO-TITE) ONOCIETE (CIVESTO-TITE) ONOCIETE (CIVESTO-TITE) MITS: CYCLE I DEPENDENT KINAKS, CYCLE IN DEPENDENT KINAKS, CHOUTEN KINAKS BURLITPUE TÜMÖR SUPPRESSOR, 3 MITS! ONOCIETE (CIVESTO-TITE) ONOCIETE (CIVESTO-TITE) ONOCIETE (CIVESTO-TITE) ONOCIETE (CIVESTO-TITE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, AI PHA META. CYMPI FY
Coumpound	GA BINDING PROTEIN ALPHA; CHARI: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	COLIN-DEPUBDIT KINASE 6; CHAIN-A: MULTIPLE E; B;	COLIN-DEPENDENT KINASE 6; CHADIA, AMLTIELE TUMOR SUPRESSOR; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; PI9INK4D; CHAIN: B;
SEQFOL D score					
PMF	1.00	1.00	1.00	0.35	1.00
Verify	0.40	0.48	0.62	0.22	0.82
Psi Blast	9.6c-40	1.3e-31	3.2e-26	8c-19	1.7e-32
END	154	157	154	121	164
STAR T AA	4	7	39	9	39
CHAI N ID	m		В	g	м
PDB ID	lawc	1bd8	1817	1617	1blx
SEQ No. 15	1257	1257		1257	1257

PDB annotation	(INHIBITOR PROTEINKINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR	_	KINASE, CELL CYCLE 2 CONTROL,	ONHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE,	HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN-	HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-	HELIX, ANKYRIN REPEAT	METAL BINDING PROTEIN ZINC-	BINDING MODULE, ANKYRIN	REPEATS, METAL BINDING	PROTEIN	METAL BINDING PROTEIN ZINC-	BINDING MODULE, ANKYRIN	REPEATS, METAL BINDING	PROTEIN	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANK YRIN REPEAT, 2 CDK 4/6	THEFTON
Coumpound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN:	B;			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;				CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	PYK2-ASSOCIATED PROTEIN	BETA; CHAIN: A;			PYK2-ASSOCIATED PROTEIN	BETA; CHAIN: A;			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;				CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;			
SEQFOL D score																																
PMF		1.00				0.88					1.00		0.95		0.80				66.0				00.1					1.00				
Verify		0.38				0.34					0.70		0.42		0.41				0.05				0.52					0.47				
Psi Blast		1.6e-30				8e-37					1.6e-26		3.2e-20		6.4e-15				1.1e-17				4.8e-36					8e-18				
END AA		157				159					154		127		91				157				158					163				
STAR T AA		4				9					30		9		7				71			1	•					73				-
CHAI N ID		В				٧					٧		Ą		Ą				٧				V					Ą				
PDB		1blx				6nq1					S S S		1d9s	,	Idea				Ideq				qui					lihb				1
SEQ UO: NO:		1257				1257					1257		1257		1257				1257				1257					1257				J

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PDB annotation	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	REGIII ATION/ANK BEPEAT	ANKYRIN 2 REPEAT HELIX	COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)	P53BP2; ANKYRIN REPEATS, SH3,	P53, TUMOR SUPPRESSOR,	MULITURINE 2 FAMILY, NUCLEAR PROTEIN BEOSMEORY ATTOM	PROTEIN, PROSPHORITATION,	DISEASE MULATION, 3	ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)	P53BP2; ANKYRIN REPEATS, SH3,	P53, TUMOR SUPPRESSOR,	MULTIGENE 2 FAMILY, NUCLEAR	PROTEIN, PHOSPHORYLATION,	DISEASE MUTATION, 3 POLYMORPHISM. COMPLEX (ANTI-			
Coumpound	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	F. P.	•	P53; CHAIN: A; 53BP2; CHAIN:	B;							P53; CHAIN: A; 53BP2; CHAIN:	· · ·					
SEQFOL D score		52.27																						
PMF	0.84		86.0	86.0	1.00	1.00				98'0								1.00						
Verify score	0.08		0.32	0.22	0.04	0.39				0.04								0.24						
Psi Blast	8e-38	3.2e-26	3.2e-26	6.4e-24	I.1e-23	I.6e-38				1.4e-19								1.6e-25						
END	162	152	156	901	164	162				92								154						
STAR T AA	4	35	40	5	74	4				12								39						
CHAI N ID	Q					œ				В								В						
PDB ID	E)[1	imyo	imyo	lmyo	lmyo	Infi				lycs								lycs						
SEQ NO:	1257	1257	1257	1257	1257	1257				1257								1257						

	<u></u>	S, S, MAR, MAR, MAR, MAR, MAR, MAR, MAR, MAR	Γ	YPE	- K		B C	-	ż	OR		GEN		_				
PDB annotation	ONCOGENE/ANKYRIN REPEATS)	ONCOGEDER (AND TREPEATS) ONCOGEDERANY RIN REPEATS) ONCOGEDERANY RIN REFEATS, SHE, PEST THWOR SUPPRESSOR, MALTITIONS 2 PAMALY, INCICLEAR REPORTS, HORSON, PORTEN, PROSEDORYLATION, DISEASE MALTATION, 3 ONPORTHING AND TANDON, PAROMERS AND MALTATION, 3 ONPORTHERS AND TANDON, PORCESSOR AND T		LECTIN CL-QPDWG; 1AFB 7 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1AFB 22	COLLAGEN BINDING PROTEIN IX- BP: IX-BP: COAGULATION FACTOR	IX-BINDING, HETERODIMER,	VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN	BINDING PROTEIN	COLLAGEN BINDING PROTEIN IX-	BP; IX-BP; COAGULATION FACTOR	IX-BINDING, HETERODIMER,	JECTIN SUPERFAMILY, COLLAGEN	MEMBRANE PROTEIN C-TYPE	ECTIN-LIKE DOMAINS		MEMBRANE PROTEIN C-TYPE		
	ő	ON PESSON ON O	L	<u> </u>	8 8		E E	Ħ	8			96	ME	9		ME	1	
Coumpound		P53; CHAIN: A, 53BP2; CHAIN: B;		MANNOSE-BINDING PROTEIN- A; IAFB 4 CHAIN: 1, 2, 3; 1AFB 5	COAGULATION FACTOR IX- BINDING PROTEIN A; CHAIN:	A; COAGULATION FACTOR IX-	BINDING PROTEIN B; CHAIN: B;		COAGULATION FACTOR IX-	BINDING PROTEIN A; CHAIN:	A; COAGULATION FACTOR IX-	B;	FLAVOCETIN-A: ALPHA	SUBUNIT; CHAIN: A;	SUBUNIT; CHAIN; B	FLAVOCETIN-A: ALPHA	FLAVOCETIN-A: BETA	SUBUNIT; CHAIN: B
SEQFOL D score				52.08					61.48									
PMF		1:00			0.11								0.89			10.0		
Verify		0.44			0.42								0.20			0.03		
Psi Blast		1.6e-22		3.4e-20	8c-34				8c-34				6.4e-28			1.4e-30		
END		161		183	180				181				185			183		
STAR		73		6	31				34				31			31		
CHAI		В		-	٧				٧				V			В		
PDB U		lycs		1afb	16j3				E[qI				lc3a			1c3a		
SEQ No en SEQ		1257		1258	1258				1258				1258			1258		_

PDB annotation	SIGNALING PROTEIN HEPATIC LECTIN HI: C-TYPE LECTIN CRD	INTIMIN INT199; INTIMIN, ESCHERICHA COLI, CELL ADHESION, OUTER MEMBRANE 2 PROTEIN, NMR SPECTROSCOPY	SUGAR BINDING PROTEIN C-TYPE LECTIN, MANNOSE RECEPTOR			CELL ADHESION IMMUNOGLOBULIN-LIKE FOLD, C- TYPE LECTIN-LIKE FOLD	LECTIN TETRANECTIN, PLASMINOGEN BINDING, KRINGLE 4, ALPHA-HELICAL 2 COILED COIL, C-TYPE LECTIN, CARBOHYDRATE RECOGNITION DOMAIN	COLLED-COIL HUP 12	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPB LECTIN, GLA- DOMAIN 2 BINDING, C-TYPB CRD MOTIF I OOP EXCHANGED DIMER	COAGITATION FACTOR BINDING
Coumpound	ASIALOGLYCOPROTEIN RECEPTOR 1: CHAIN: A:	INTIMIN; CHAIN: I;	MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	CELL ADHESION PROTEIN E- SELECTIN (LECTIN AND BGF DOMAINS, RESIDUES 1 - 157) IESL 3 (FORMERLY KNOWN	TAS ELAMON IN THE CELL ADTHESION PROTEIN E. SELECTIN (LECTIN AND EGF DOMAINS, RESDUES 1 - 157) IESLS (PORMERLY KNOWN AS ELAM-1) IESL, 4	INTIMIN; CHAIN: I;	TETRANECTIN, CHAIN: NULL;	MANNOSE-BINDING PROTEIN; 1HUP 4 CHAIN; NULL; 1HUP 5	COAGULATION FACTORS IXX-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGIT ATION FACTORS
SEQFOL D score					60.26		19:89	50.48		58.55
PMF score	99.0	0.57	0.36	0.89		0.40			0.21	
Verify	0.72	-0.69	0.41	0.45		61.0-			0.21	
Psi Blast	6.4e-28	0.0093	1.6e-29	4.8e-30	4.8e-30	0.0093	1.36-23	6.4e-21	4.8e-32	4.8e-32
END	180	08	187	213	220	08	184	183	081	181
STAR T AA	31	52	29	4	45	52	12	∞	31	34
CHAI	V		m			н			<	V
PDB CI	1dv8	le5u	legg	<u>8</u>	lesi	100	Ihm	1hup	lix	1
SEQ ID	NO:	1258	1258	1258	1258	1258	1258	1258	1258	1258 1ixx

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PDB annotation	IXX-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA- DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING IXX-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA- DOMAIN 2 BINDING, C-TYPE CRD MOTTE, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING IXX-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA- DOMAIN 2 BINDING, C-TYPE CRD MOTTF, LOOP EXCHANGED DIMER	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE		LECTIN TETRANECTIN, PI ASMINOGEN BINDING KRINGI R
Coumpound	IXX-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTORS IXX-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COA GULATION FACTORS IXX-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	LITHOSTATHINE; CHAIN: NULL	LITHOSTATHINE; CHAIN: NULL	LITHOSTATHINE; CHAIN: A;	LITHOSTATHINE; CHAIN: A;	LECTIN MANNOSE-BINDING PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) IRTM 3 IRTM 96	TETRANECTIN; CHAIN: NULL;
SEQFOL D score			53.06		71.84	72.35		50.72	59.80
PMF		0.45		0:30			0.52		
Verify		0.24		0.51			0.65		
Psi Blast		1.36-29	1.36-29	1.6e-31	1.66-31	1.6e-31	1.6e-31	5.1e-19	1.2e-24
END		183	183	182	183	183	182	183	184
STAR T AA		31	34	31	31	18	31	6	28
CHAI N ID		æ	В			<	<	_	
PDB D		lix	lix	1111	Ħ	Iqdd	1qdd	1rtm	1tm3
SEQ NO:		1258	1258	1258	1258	1258	1258	1258	1258

PDB annotation	4, C-TYPE LECTIN, 2 CARBOHYDRATE RECOGNITION DOMAIN	ANTIFREEZE PROTEIN RECOMBINANT SEA RA VEN PROTEIN, SOLUTION BACKBONE FOLD, C-2 TYPE LECTIN, ANTIFREEZE PROTEIN	OXIDOREDUCTASE DAPDH; NADP, DEHYDROGENASE, D-AMINO ACID DEHYDROGENASE, LYSINE 2	BIOSYNTHESIS, ASYMMETRIC DIMER, OXIDOREDUCTASE							COMPLEX (PROTEASE INHIBITOR/PEPTIDE) PAI-1: SERINE	PROTEASE INHIBITOR, PAI-1,	CARBOHYDRATE, INHIBITOR 2 COMPLEX, PEPTIDE	SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR,
Coumpound	7	SEA RAVEN TYPE II ANTIPREEZE PROTEIN; CHAIN: F A;	DIAMINOPIMELIC ACID DEHYDROGENASE; CHAIN: A, II B;		ADS(A)-	GLYCERALDEHYDE-3- PHOSPHATE	DEHYDROGENASE (E.C.1.2.1.12) 3GPD 4	OXIDOREDUCTASE (/NAD\$(A)-	GLYCERALDEHYDE-3- PHOSPHATE	DEHYDROGENASE (E.C.1.2.1.12) 3GPD 4	PLASMINOGEN ACTIVATOR INHIBITOR TYPE 1: CHAIN: A:			ANTICHYMOTRYPSIN; CHAIN: S A, B;
SEQFOL D score					491.59						115.78			
PMF		0.54	0.13					1.00						96:0
Verify		-0.06	-0.51					0.93						0.25
Psi Blast		1.6e-27	4.8e-05		0			0			4.8e-91			0
END		179	33		336			336			463			430
STAR		59	_		2						82			88
CHAI N ID		V V	¥		×			~			٧			V
PDB		2afp	Idap		3gpd			3gpd			la7c			las4
SEQ NO D		1258	1259		1259			1259			1263			1263

PDB annotation	ANTICHYMOTRYPSIN	IN: SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR, ANTICHYMOTRYPSIN		I	R PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING	R PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING	MIN: HYDROLASE INHIBITOR SERPIN FOLD, RCI. CLEAVAGE A BETA	SHEET POLYMERISATION	R HYDROLASE INHIBITOR NATIVE SERPIN, HYDROLASE INHIBITOR	HYDROLASE/HYDROLASE	COMPLEX SERPIN ALPHA-1-	ANTITRYPSIN, 2 TRYPSIN											
Coumpound		A, B;	HUMAN ANTITHROMBIN-III ANTITHROMBIN III 1ATH 3	HUMAN ANTITHROMBIN-III ANTITHROMBIN III IATH 3	PLASMINOGEN ACTIVATOR INHIBITOR-2: CHAIN: A:	PLASMINOGEN ACTIVATOR INHIBITOR-2; CHAIN: A:	PI-ARG ANTITRYPSIN; CHAIN: A: PI-ARG ANTITRYPSIN:	CHAIN: B;	PLASMINOGEN ACTIVATOR INHIBITOR-1: CHAIN: A. B.	ALPHA-1-ANTITRYPSIN;	CHAIN: A; ALPHA-1- ANTITRYPSIN: CHAIN: B:	TRYPSIN; CHAIN: C;	HYDROLASE	INHIBITOR(SERINE PROTEINASE) HORSE	LEUKOCYTE ELASTASE	INHIBITOR (HLEI) 1HLE 3	HYDROLASE	INHIBITOR(SERINE	PROTEINASE) HORSE	LEUKOCYTE ELASTASE	INHIBITOR (HLEI) IHLE 3	SERPIN OVALBUMIN (EGG	ALBUMIN) IOVA 3
SEQFOL D score		104.85	102.92			101.02			120.11								84.90					126.84	
PMF score				1.00	1.00		0.04			0.80			1.00										
Verify				0.23	89.0		-0.75			0.23			0.38										
Psi Blast		0	1.3e-96	1.3e-96	0	0	1.3e-09		3.2e-94	0			3.2e-98				3.2e-98					0	
END		438	464	464	463	463	463		463	432			426			_	432					463	
STAR		06	101	82	98	98	433		83	98			58				82					œ	
CHAI N ID		Ą	m	ш	¥	¥	В		٧	¥			V				٧					∀	
PDB		las4	lath	lath	1by7	1by7	1d5s		1db2	lezx			Ihle				lhle					Iova	
SEQ O.S.		1263	1263	1263	1263	1263	1263		1263	1263			1263				1263					1263	

PDB annotation		SERINE PROTEASE INHIBITOR, ALPHA-1-PROTEINASE INHIBITOR,	ALPHA-1-ANTIPROTEINASE;	SERPIN, GLYCOPROTEIN, SIGNAL, 2	POLYMORPHISM, EMPHYSEMA,	DISEASE MUTATION, ACUTE PHASE	SERINE PROTEASE INHIBITOR	ALPHA-I-PROTEINASE INHIBITOR,	ALPHA-I-ANTIPROTEINASE;	SERINE PROTEASE INHIBITOR,	SERPIN, GLYCOPROTEIN, SIGNAL, 2	POLYMORPHISM, EMPHY SEMA,	DISEASE MUTATION, ACUTE	CHASE	AI PHA-I-PROTEINASE INHIBITOR	AT PHA-I-DI-SERDIN ANTITED VIDEN	POLYMER, CLEAVED	SERPIN AACT SERPIN. SERINE	JN: PROTEINASE INHIBITOR, PARTIAL	LOOP 2 INSERTION, LOOP-SHEET	POLYMERIZATION, EMPHYSEMA.	DISEASE 3 MUTATION, ACUTE	PHASE PROTEIN,	CONFORMATIONAL DISEASE	SERINE PROTEASE INHIBITOR	SERINE PROTEASE INHIBITOR,	SERPIN, PROTEASE	<u> </u>	INHIBITOR	
Coumpound	ALBUMIN) IOVA 3	ALPHA-1-ANTITRYPSIN; CHAIN: A;					ALPHA-1-ANTITRYPSIN;	CHAIN: A;						AT DUTA 4 AD PROPERTY APPOINT	CHAIN: A B:	67 5111111111111111111111111111111111111		ALPHA-1-	ANTICHYMOTRYPSIN; CHAIN:	A;					SERPIN K; CHAIN: NULL;			ANTITHROMBIN; CHAIN: L, I;		
SEQFOL D score							146.76																		102,05			139.88		
PMF		1.00												21.0	71.0			1.00												
Verify		0.49												200	2			0.44												
Psi Blast		0					0							00.00	1.00-07			0							3.2e-85			0		
END		463					466							679	2			464							463			466		,,,,
STAR		98					88							422	2			88							08			47		40
CHAI N ID		Ą					<							9	1			A										_		
PDB ID		dþ1					Iqp							Tomp	anh.			Idmn							1sek			2ant		
S B SE		1263					1263							1361	3			1263							1263			1263		1,001

ion		KIN,	RIN,	EPTIDE) B35; TBILITY	HLA-B3501,		EPTIDE) B35; TBILITY	ILA-B3501,		EPTIDE) B35;	BILITY	-ILA-B3501,		COMPLEX	B8, HIV,		COMPLEX		COMPLEX	B8, H∐V,	COMMITTEN	COMITTE	COMPLEX	B8, HIV,
PDB annotation	INHIBITOR	SERPIN SERPIN, HEPARIN, INHIBITOR	SERPIN SERPIN, HEPARIN, INHIBITOR	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY	ANTIGEN, MHC, HLA, HLA-B3501,	(ANTIGEN/PEPTIDE)	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY	ANTIGEN, MHC, HLA, HLA-B3501,	HIV, 2 NEF, COMPLEX	COMPLEX (ANTIGEN/PEPTIDE) B35;	MAJOR HISTOCOMPATIBILITY	ANTIGEN, MHC, HLA, HLA-B3501,	HIV, 2 NEF, COMPLEX	HISTOCOMPATIBILITY COMPLEX	B8; B2M; PEPTIDE HLA B8, HIV,	MHC CLASS 1,	HISTOCOMPATIBILITY COMPLEX		HISTOCOMPATIBILITY COMPLEX	BS; BZM; PEP LIDE HLA BS, HIV,	HISTOCOM A TIBILITY COMMITS	rusi occivir Attbictiti	HISTOCOMPATIBILITY COMPLEX	B8; B2M; PEPTIDE HLA B8, HIV,
Coumpound		ANTITHROMBIN; CHAIN: L, I;	ANTITHROMBIN; CHAIN: L, I;	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;			B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;			B*3501; CHAIN: A, B; PEPTIDE	VPLRPMTY; CHAIN: C;			B*0801: CHAIN: A: BETA-2	MICROGLOBULIN; CHAIN: B;	HIV-1 GAG PEPTIDE	(GGKKKYKL - INDEX	PEPTIDE); CHAIN: C;	B*0801; CHAIN: A; BETA-2	MICKOGLOBOLIN; CHAIN; B;	AGENT INVAVIOUS	PEPTIDE); CHAIN: C;	B*0801; CHAIN: A; BETA-2	MICROGLOBULIN; CHAIN: B;
SEQFOL D score		125.53					237.20												239.77					
PMF			1.00	00.1						1.00				8								•	1.00	
Verify			0.63	0.93						1.19				0.97									96.0	
Psi Blast		0	0	6.4e-92			1.2e-93			1.2e-93				3.2e-92					3.2e-92				8.5e-92	
END		466	464	218			219			210				218					219				210	
STAR T AA		65	81	25			25			26				25					25				26	
CHAI N ID		7	L	⋖			A			A				A					٧				A	
EDB EDB		2ant	2ant	lalı			laln			laln				lacd	,				lagd				lagd	
SEQ No.		1263	1263	1264			1264			1264				1264					1264				1264	

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PDB annotation		HISTOCOMPATIBILITY COMPLEX	IMMUNE SYSTEM	IMMUNOGLOBULIN FOLD				IMMUNE SYSTEM MHC, HLA,	CLASS I, KIR, NK CELL RECEPTOR,	IMMUNOGLOBULIN 2 FOLD,	RECEPTOR/MHC COMPLEX				IMMUNE SYSTEM MHC, HLA,	CLASS I, NIK, NR CELL RECEPTOR,	IMMUNOGLOBULIN 2 FOLD,	RECEPTOR/MHC COMPLEX																
Coumpound		(GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HLA-A*0201; CHAIN: A, D;	BETA-2 MICROGLOBULIN;	COMES D. D. DILLY-1	OCIAMERIC IAX PEPTIDE;	CHAIN: C, F;	HLA-CW3 (HEAVY CHAIN);	CHAIN: A; BETA-2-	MICROGLOBULIN; CHAIN: B;	PEPTIDE FROM IMPORTIN	ALPHA-2; CHAIN: C; NATURAL	KILLER CELL RECEPTOR	KIR2DL2; CHAIN: D, E;	HLA-CW3 (HEAVY CHAIN);	CHAIN: A; DE IA-2-	MICROGLOBULIN; CHAIN: B;	PEPTIDE FROM IMPORTIN	ALPHA-2; CHAIN: C; NATURAL	KILLER CELL RECEPTOR	KIR2DL2; CHAIN: D, E;	HISTOCOMPATIBILITY	ANTIGEN MURINE CLASS I	MAJOR HISTOCOMPATIBILITY	COMPLEX CONSISTING 1HOC 3	OF H-2D==B==, B2-	MICROGLOBULIN, AND A 9-	RESIDUE PEPTIDE 1HOC 4	HISTOCOMPATIBILITY	ANTIGEN HUMAN CLASS I	HISTOCOMPATIBILITY	ANTIGEN 1HSA 3 /HLA-	B(ASTERISK)27055 1HSA 4	THOUGHT THE PARTY MANY
SEQFOL	D score																					206.63												221 22
PMF	score		1.00					1.00							1.00														1.00					
Verify	score		1.03					1.13							1.29														0.91					_
Psi Blast			1.6e-88					9.6e-91							8.5e-93							1.6e-84							3.2e-91					3.20-01
END	Ψ¥		218					218							210							218							218					210
STAR	TAA		25					53							56							25							25					25
CHAI	e z		. ¥					∢							٧							٧							٧					V
PDB	e e		1duz				,	lefx				_			Iefx							Ihoc							lhsa					PSS
SEQ	Q Ö		1264					1264							1264							1264							1264					1264

PDB annotation				MOOR HISTOCOMATIBILITY COMPLEX MHC NONCLASSICAL CHAIN MHC.E, ELLAE, MHC CLASS HACE, HIA, E, MAN HISTOCOMATIBILITY COMPLEX, MHC, HA, 2 BRITS MICROGLOBULIN, PETTIBE, LEADER PETTIBE, 3 NON- CLASSICAL, MHC, CLASSI BMHC CLASSICAL, MHC, CLASSI BMHC	IMAUNE SYSTEM IMAUNOGLOBULIN ((G)-LIKE IMAUNOGLOBULIN (G)-LIKE DOWAIN, ALP'H FELIX, BETA SHEET, 2 IMAUNE SYSTEM	
Coumpound	ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA- B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW 8.1 (LEUCOCYTE 1HSB 3	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 114SB 3 ANTIGEN) 114SB 4	HSTOCOMPATIBLITY HISTOCOMPATIBLITY ANTICEN HA-E; CHANF; A, C; ERY-S-MICROGLOBULN; CHANF, B, PEPTIDE (VMAPRITUL); CHAIN: P, Q;	HISTOCOMPATIBILITY LBUKOCYTB ANTIGEN (HLA)- CW4 CHANI: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HITMAN CLASS I
SEQFOL D score			226.78	209.47		257.75
PMF		1.00			8:	
Verify score		1.15			1.17	
Psi Blast		3.2e-89	3.2e-89	4.8c-88	6.4e-89	9.6e-81
END		218	219	219	218	199
STAR T AA		25	25	26	26	25
CHA1 N ID		¥	∢	¥.	∢	4
EDB ED		1hsb	Ihsb	Imhe	Iqqd	Itmc
S e S		1264	1264	1264	1264	1264

PDB annotation		COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MFC, HLA, HLA-B3501, HLY, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	COMPLEX (ANTIGEN/PEPTIDE) B35, MAJOR HISTOCOMPATIBILITY ANTIGEN, MHG, HLA, HLA-B3501, HIV, 2 NET, COMPLEX (ANTIGEN/PEPTIDE)	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	IMMUNE SYSTEM MHG, HLA, CLASS, IKR, NK CELLA RECEPTOR, IMMUNOGLOBULIN 2 POLD, RECEPTOR/MHC COMPLEX.	
Coumpound	HISTOCOMPATIBILITY ANTIGENHIA-AW68 ITMC3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC4	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: G;	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE): CHAIN: C:	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE): CHAIN: C:	HLA-CW3 (HEAVY CHAIN); CHAIN, A, BETA-2. MICROGLOBULIN; CHAIN; B; PEPTIDE FROM IMPORTIN ALPIRA-2; CHAIN; C, NATURAL KILLER CELL RECEPTOR	HISTOCOMPATIBILITY
SEQFOL D score			222.84		242.14		
PMF		1.00		00'1		9.1	00.1
Verify		0.82		0.93		0.96	1.04
Psi Blast		0	0	0	0	4.8e-100	1.6e-100
END		212	213	212	213	212	212
STAR		25	25	25	25	8	25
CHAI N ID		4	V.	4	∢	4	Ą
PDB ID		laln	laln	lagd	lagd	lefx	Thsa
SEQ No: D		1265	1265	1265	1265	1265	1265

		IMANUNE SYSTEM IMANUNCOLOBULIN ((G)-LIKE DOMAIN, ALPIA, HELIX, BETA SHEET, 2 IMANUNE SYSTEM			COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY
ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY 'ANTIGEN 1HSA 3 /HLA- B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY ANYIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 115A 3 / FLA- BASTIERNZYJOSS 115A 4	HISTOCOMPÁTIBILITY LEUKOCYTE ANTIGEN (FLA)- CWA CHAIN A; BETA-2 MICROGLOBULIN; CHAIN: B; HIACW4 SPECIFIC PEPTIDE; CHAIN: C;	ANTIGEN TRUNCATED HUMAN CLASS I HUMAN CLASS I HUMAN CLASS I ANTIGEN HLA-AW68 ITMC3 COMPLEXED WITH A COMPLEXED WITH A GENABLE PEPTIDE GENABLE PEPTIDE GENABLE TRENTEN HANTIGEN HITH A HUMAN THE A HUMAN	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HUSTOCOMPATIBILITY ANTIGEN HAA-WKS ITMC 3 DECAMERCE PITTE EVAPORATE OF THE ATTENCY	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;
	212.48			245.23	
		1.00	00:		1.00
		0.83	00:1		0.88
	1.6e-100	1.3e-98	3.2e-93	3.2e-93	4.8e-97
	213	212	199	199	210
	25	26	25	25	22
	٧	V V	A	٧	e e
	Ihsa	Iqqd	Itmc	Itmc	laIn
	1265	1265	1265	1265	1266
	ANTIGONAL MASS I HATTOCOMPATHELLTY ANTIGONAL MISA, AILA-A BASTERRENZONAL MISA, AILA-A BASTERRENZONAL MISA, AILA-A	Thus A 25 213 1.6e-100 212.48	ANTIGEN HUMAN CLASS	ANTIGEN HUMAN CLASS	A

01.	STAR T AA	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
								ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PETTIDE)
22	_	210	4.8e-97			202.13	B*3501; CHAIN; A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY
								ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
22		210	1.le-97	0.92	1.00		B*0801; CHAIN: A; BETA-2	HISTOCOMPATIBILITY COMPLEX RS: BOM: DEPTIDE HT A RS: HIV
							HIV-1 GAG PEPTIDE	MHC CLASS I,
							(GGKKKYKL - INDEX PEPTIDE); CHAIN; C;	HISTOCOMPATIBILITY COMPLEX
22	1.	210	1.1e-97			212.14	B*0801; CHAIN: A; BETA-2	HISTOCOMPATIBILITY COMPLEX
							MICROGLOBULIN; CHAIN: B;	B8; B2M; PEPTIDE HLA B8, HIV,
							(GOKKKYKL - INDEX	HISTOCOMPATIBILITY COMPLEX
	_						PEPTIDE); CHAIN: C;	
22		208	4.8e-95	0.88	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
							CHAIN: B, E; HTLV-1	
							OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	
22	\vdash	210	3.2e-96	1.08	1.00		HLA-CW3 (HEAVY CHAIN);	IMMUNE SYSTEM MHC, HLA,
							CHAIN: A; BETA-2-	CLASS I, KIR, NK CELL RECEPTOR,
							MICROGLOBULIN; CHAIN; B;	IMMUNOGLOBULIN 2 FOLD, PECEPTOR ACHC COART EX
	_						ALPHA-2: CHAIN: C: NATURAL	
	_						KILLER CELL RECEPTOR	
	-						KIR2DL2; CHAIN: D, E;	
22	_	210	3.2e-96	0.89	00.1		HISTOCOMPATIBILITY ANTIGEN HIMAN CLASS 1	
							HISTOCOMPATIBILITY	
	_						ANTIGEN 1HSA 3 /HLA-	

PDB annotation																		IMMUNE SYSTEM	IMMUNOGLOBULIN (IG)-LIKE	DOMAIN, ALPHA HELIX, BETA	SHEET, 2 IMMUNE SYSTEM											
Coumpound	B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY	ANTIGEN HUMAN CLASS I	ANTIGEN 14SA 3 (41 A-	B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY	ANTIGEN CLASS I	HISTOCOMPATIBILITY	ANTIGEN A W68.1	(LEUCOCYTE 1HSB 3	ANTIGEN) 1HSB 4	HISTOCOMPATIBILITY	ANTIGEN CLASS I	HISTOCOMPATIBILITY	ANTIGEN A W68.1	(LEUCOCYTE 1HSB 3	ANTIGEN) 1HSB 4	HISTOCOMPATIBILITY	LEUKOCYTE ANTIGEN (HLA)-	CW4 CHAIN: A; BETA-2	MICROGLOBULIN; CHAIN: B;	HLA-CW4 SPECIFIC PEPTIDE;	HISTOCOMPATIBILITY	ANTIGEN TRUNCATED	HUMAN CLASS I	HISTOCOMPATIBILITY	ANTIGEN HLA-AW68 1TMC 3	COMPLEXED WITH A	DECAMERIC PEPTIDE	(EVAPPEYHRK) 1TMC 4	HISTOCOMPATIBILITY	ANTIGEN TRUNCATED
SEQFOL D score		195.27										189.34																			228.77	
PMF						1.00												1.00					1.00									
Verify						0.87												0.89					86.0									
Psi Blast		3.2e-96				4.8e-96						4.8e-96						3.2e-94					4.8e-90								4.8e-90	
END		210				208						210						210					197								197	
STAR		22				22						22						23					22								22	
CHAI N ID		٧				4	:					٧						٧					Ą								٧	
en En		Thsa				lhsb						Ihsb						1qqd					Itmc								Itmc	
Se Se Se		1266				1266						1266						1266					1266								1266	

PDB annotation	IMMUNOGLOBULIN 2 FOLD, RECEPTORMHC COMPLEX					MAMUNE SYSTEM MAMUNGOLOBULIN (1G)-LIKE DOMAIN, ALPIA HELIX, BETA SHEET, 2 IMMUNE SYSTEM	
Coumpound	MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIRZDI.2; CHAIN: D, E;	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA- B(ASTERISK) Z7058 1HSA 4	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHSA 3 /HLA- RASTERISK) Z7055 IHSA 4	HISTOCOMPATIBILITY ANTIGEN CLASS! HISTOCOMPATIBILITY ANTIGEN AW®! (LEUCOCYTE HISB 3 ANTIGEN) HISB 4	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW8.1 ANTIGEN AW8.1 ANTIGEN AW8.1 ANTIGEN AW8.1	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	HISTOCOMPATIBILITY
SEQFOL D score			198.64		190.28		
PMF		1.00		1.00		1.00	I.00
Verify		1.02		0.98		0.95	0.91
Psi Blast		1.6e-99	I.6e-99	I.1e-98	I.Ie-98	4.8e-97	6.4e-91
END AA		214	214	214	214	214	200
STAR T AA		25	25	25	25	26	25
CHAI N 1D		∢	∢	٧	4	٧	A
E G		lhsa	Ihsa	lbsb	thsb	Iqqd	Itmc
SEQ NO.		1267	1267	1267	1267	1267	1267

PDB annotation	HISTOCOMPATIBILITY COMPLEX	IMMUNE SYSTEM FC IGG PHAGE DISPLAY PEPTIDE	IMMUNOGLOBULIN FOLD	IMMUNE SYSTEM MHC, HLA, CLASS, KIR, NR CELL BRCEPTOR, IMMUNOGIOBULIN 2 FOLD, RECEPTORMHC COMPLEX			
Coumpound	(GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	IMMUNOGLOBULIN LAMBDA HEAVY CHAIN; CHAIN: A, B; ENGINEERED PEPTIDE; CHAIN: E, F;	HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C. E:	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBILIN: CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR	KIRZDIZ, CHAIN: D. E. HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HISA HUMAN CLASS I ANTIGEN HAS A HILA-	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 195A 3 /HLA- ANTIGEN 195A 3 /HLA-	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LBUCOCYTE HISB 3 ANTIGEN) HISB 4
SEQFOL D score						381.68	
PMF		0.00	1.00	1.00	1.00		0.00
Verify		-0.28	0.83	0.83	0.80		0.82
Psi Blast		0.00034	0	0	0	0	0
END		314	300	303	301	301	295
STAR T AA		224	25	શ	25	25	25
CHAI N ID		<	∢	<	<	<	<
FDB ID		1dn2	Iduz	Tefx 1	1hsa	Ihsa	lhsb
SEQ NO ID		1268	1268	1268	1268	1268	1268

PDB annotation		IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN			IMMUNE SYSTEM IMMUNG GOLOBULIN (GG)-LIKE DOMAIN, ALPHA HELDY, BETA SHEET, 2 IMMUNE SYSTEM	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC; HLA, HLA-B3501, HNT, 2 NBC, COMPLEX (ANTIGEN/PEPTIDE)	COMPLEX (ANTIGEMPEPTIDE) B35, MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NBF, COMPLEX (ANTIGEMPEPTIDE)
Coumpound	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW8.1 (LEUCOCYTE HSB 3 ANTIGEN 1188 4	IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN IMMUNOGLOBULIN GI (IGGI) (MCG) WITH A HINGE DELETION IMCO 3	IMMUNOGLOBULIN IMMUNOGLOBULIN GI (IGGI) (MCG) WITH A HINGE DELETION IMCO 3	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (FLA)- CW4 CHAIN: A; BETA-2 MICKOGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C,	B*3301; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;
SEQFOL D score	416.11						279.39
PMF		0.71	0.23	0.48	1.00	0.1	
Verify		0.26	0.09	0.30	0.63	0.88	
Psi Blast	0	1.6e-05	1.7e-05	6.8e-06	0	0	0
END	295	308	310	314	299	285	288
STAR T AA	23	224	681	220	26	25	25
CHAI N ID	<	Я	н	щ	¥	▼	<
PDB ID	Ihsb	ligt	Ітсо	Птео	pbbI	IaIn	lain
SEQ NO:	1268	1268	1268	1268	1268	1269	1269

PDB annotation	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	HISTOCOMPATIBILITY COMPLEX B8, B2M, PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	IMMUNOGLOBULIN FOLD	DAMING SYSTEM MIC, HLA, CLASS I, KIR NK CELL RECEPTOR, MANINOGLOBULIN 2 FOLD, RECEPTORAHIC COMPLEX			
Coumpound	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTITIN: CHAIN: C.	B'0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - NDEX PEPTIDE): CHAIN: C:	HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E, HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2. MCROGLOBULIN; CHAIN: B; PETTIDE FROM IMPORTIN ALPHA-2; CHAIN: C NATURAL KILLER CELL RECEPTOR KIRZDL2; CHAIN: D, E:	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HISA 3 /HLA- BASTERISK 27058 HSA 4	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA- BASTIRENZYSOS HSA 4	HISTOCOMPATIBILITY ANTIGEN CLASS I
SEQFOL D score		278.31				284.65	
PMF	00:1		00.1	0.1	00.1		1:00
Verify score	0.87		0.93	0.94	0.93		0.83
Psi Blast	0	0	0	0	0	0	0
END	285	288	285	285	285	288	285
STAR	25	22	25	25	25	25	25
CHAI N ID	<	⋖	<	<	∢	Y	∢
aa. D	lagd	lagd	Iduz	lefx	lhsa	lhsa	1hsb
SEQ NO:	1269	1269	1269	1269	1269	1269	1269

					1
PDB annotation			MADOR HISTOCHAPTIBILITY COMPLEX MEO NONCLASSICAL COMPLEX MEO NONCLASSICAL ELAN, MECE, HI A.E., MHC CLASS HILAC, HIAC, B.MAOR HISTOCHOWATIBILITY COMPLEX, MICHOGLOBULIN, PEPTING, ELANGE PEPTING, STARRED SANDER CLASSICAL MEC CLASSIC BARGO CLASSICAL MEC CLASSIS BARGO CLASSICAL MEC CLASSIS	ANOR HENCOMATHELITY COMPLEX MEC NONCLASSIGAL COMPLEX MEC BLACE, HIACE, H	IMAUNE SYSTEM IMAUNOGCOBULINE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
Commpound	HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) 1HSB 4	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW8.1 ANTIGEN AW8.1 ANTIGEN IHSB 3	HISTOCOMPATIBILITY ANTIGEN HIA-E; CHAIN: A, C; THATA-SAMCROGLOBULIN; CHAIN: B, D; PEFFILIS (WAAPRIVILL); CHAIN: F, Q;	HISTOCOMPATIBILITY HISTOCOMPATIBILITY ACTION HASE CHAINE A.C. BETAZ-AMICROGLOBULIN; CHAINE B. P. PEPTIDE (WMAPRIVLL); CHAINE B. Q;	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (FLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;
SEQFOL D seore		302.23		253.44	
PMF			1.00		I.00
Verify score			0.70		0.86
Psi Blast		0	0	0	0
END		288	285	288	285
STAR T AA		25	26	36	26
CHAI N ID		¥	¥.	¥.	V
PDB ID		lhsb	Imhe	Imbe	Iqqd
SEQ NO:		1269	1269	1269	1269

PDB annotation			COMPLEX (ANTIGENPEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGENPEPTIDE)	COMPLEX (ANTIGEN/PEPTIDE) B35, MAJOR HISTOCOMPATIBILITY ANTIGEN, MIC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	COMPLEX (ANTIGEN/PEPTIDE) B35, MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV,
Coumpound	HISTOCOMPATBILITY ANTGEN TRUNCATED HUMAN CLASS I HTSTOCOMPATBILITY ANTGEN H.AAWS ITMC3 COMPLEXED WITH A CO	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS II HISTOCOMPATIBILITY ANTIGEN HLA-AWS ITMC3 OMPLEXED WITH A DECAMENCE PETIDE (EVAPPETHEG) ITMC4	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C,	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B;
SEQFOL D score		257.46		239.16		
PMF	1.00		00.1		I.00	1.00
Verify	0.97		0.95		1.03	1.03
Psi Blast	80-88	86-88	1.4e-94	5,Ie-96	5.1e-96	3.2e-95
END	200	200	218	219	210	218
STAR T AA	22	25	25	25	26	25
CHAI	A	V V	∢	₹	∢	V
PDB ID	1tmc	Itmc	laln	laIn	laIn	lagd
SEQ No: D	1269	1269	1271	1271	1271	1271

PDB annotation	MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	TA-2 HISTOCOMPATIBILITY COMPLEX HAIN: B; B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	A, D; IMMUNOGLOBULIN FOLD ULIN; IMMUNOGLOBULIN FOLD PTIDE;	HAIN; Induline System Aleic, HIA, CLASSI, KIR, NR CELL, RECGETOR, RTIN, RECEPTORMHIC COMPLEX, AVITURAL PROPERTOR ALICE COMPLEX AVITURAL PROPERTOR ALICE COMPLEX ST. C.	AIN); IMATINE SYSTEM AUIC, HLA, ALMADING SYSTEM AUIC, HLA, CLASSI, KIR, NK CELL RECEPTOR, RITIN RECEPTOR/MHC COMPLEX. AATURAL STORY	7. AASS 1 7. Y. 184 4	Α.
Commpound	(GGKKKYKL - INDEX PEPTIDE); CHAIN: C:	B*0801; CHAIN: A; BETA-2 MCROGLOBULIN; CHAIN: B; HIV-I GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C:	HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, B; HTLV-1 OCTAMERIC TAX PEPTIDB; CHAIN: C, F;	HLA-CW3 (HEAVY CHAIN); CHAIN, A; BETA-2- MCROGLOBULIN; CHAIN; B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN; C; NATURAL KILLER CELL RECEPTOR KIRZDL2; CHAIN; D, B.	HLA-CW3 (HEAVY CHAIN); CHAIN, A; BETA-2. MICROGLOBULIN; CHAIN; B; PEPTIDE FROM IMPORTIN ALIPHA-2; CHAIN; C, NATURAL KILLER CELL RECEPTOR KRRZDIZ; CHAIN; D, E.	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN INSA 3 /HLA- BASTERISK/27058 IHSA 4	HISTOCOMPATTRIT ITV
SEQFOL D score		243.91					235.85
PMF			1.00	1.00	1.00	1.00	
Verify			0.93	0.95	1.16	66:0	
Psi Blast		3.2e-95	3.2e-91	1.6e-93	1e-95	4.8e-94	4.8e-94
END AA		219	218	218	210	218	219
STAR		25	25	23	26	25	25
CHAI N ID		<	∢	∢	∢	⋖	4
PDB OI		lagd	Iduz	lefx	lefx	Ihsa	Thsa
SEQ NO.		1271	1271	1271	1271	1271	1271

PDB annotation				COMPLEX STORY THE LITY COMPLEX WICH ONO PLANS ICAL COMPLEX WICH ONO PLANS ICAL COMPLEX WAS THANK WHO CLASS HANK HANK HANK THE WANK HISTOCOMPHENT TO COMPLEX, MICROGLOBULIN, PEPTIDE, LABORE PEPTIDE, CLASSER STORY HANK CLASS IS MHC CLASSICAL MHC, CLASS IS MHC	AND AND RESTORAGE ATTEMPT OF A STREAM OF A	IMMUNE SYSTEM
Coumpound	HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA- B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW8.1 ANTIGEN AW8.1 ANTIGEN) 1HSB 3	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW88.1 (LEUCOCYTE HISB 3 ANTIGEN) HISB 4	HAC CLASSI HISTOCONIVATIBILITY HISTOCONIVATIBILITY BETTA-2-MICROGLOBULIN; CHAIN: B. D; PEFTIDE (WAAPETVIL); CHAIN: P, Q;	HISTOCONPATIBILITY HISTOCONPATIBILITY HISTOCONPATIBILITY GHAINE, GHAINE, A, C, GHAINE, B, P, PEPTIDE (WAAPRIVIL), CHAINE P, Q;	HISTOCOMPATIBILITY
SEQFOL D score			238.52		218.16	
PMF		1.00		1.00		1.00
Verify		1.11		0.94		0.95
Psi Blast		4.8e-92	4.8e-92	1.6e-92	1.6e-92	1.6e-92
END		218	219	218	219	218
STAR T AA		25	23	56	92	26
CHAI		< .	∢	¥.	∢	٧
EDB CI		Ihsb	Ihsb	Imhe	Imbe	Iddd
SEQ No.		1271	1271	1271	1271	1271

PDB annotation	IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM		COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MAIC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	HISTOCOMPATIBILITY COMPLEX B8; BZM; PBPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	HISTOCOMPATIBILITY COMPLEX B8; BZM; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
Coumpound	LEUKOCYTE ANTIGEN (HLA)- CWA CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CWA SPECIFIC PEPTIDE; CHAIN: C;	ANTIGEN TRUNCATED ANTIGEN TRUNCATED HUMAN CLASS I HUMAN CLASS I ANTIGEN HLA-AW68 TMC 3 COMPLEXED WITH A DECAMENIC PETIDE (EVAPPETHRE) ITMC 4	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*3301; CHAIN: A, B; PEPTIDE VPLRPMIY; CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAQ PEPTIDE (GGKK YKL - INDEX PEPTIDE); CHAIN: C;
SEQFOL D score		267.94		150.68		152.02
PMF			1.00		1.00	
Verify			0.92		0.79	
Psi Blast		1.4c-83	8e-91	8e-91	3.2e-91	3.2e-9]
END AA		199	213	213	213	213
STAR T AA		25	25	Я	25	25
CHAI N ID		A	¥	∢	∢	4
PDB ID		ltmc	laIn	laIn	lagd	lagd
SEQ No.		1271	1272	1272	1272	1272

PDB annotation	IMMUNGELOBULIN FOLD	IMMUNE SYSTEM MHC, FILA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTORMHC COMPLEX				
Coumpound	HLA-A*0201; CHAIN: A, D; BETA-2 MCROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F:	HIA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2. CHAIN: A; BETA-2. PEPTIDE FROBULIN: B; PEPTIDE FROM IMPOSTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KILLER CELA RECEPTOR	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 118A 3 /HLA- ANTIGEN 118A 3 /HLA-	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HSA 3 /HLA- ANTIGEN HSA 3 /HLA-	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW8.1 (LEUCOCYTE IHSB 3 ANTIGEN IHSB 4	HISTOCOMPATIBILITY ANTIGEN CLASSI ANTIGEN AW68.1 GLEUCOCYTE HISB 3 ANTIGEN HISB 4 ANTIGEN) HSB 4
SEQFOL D score				151.46		178.43
PMF	00:1	00:1	1.00		1.00	
Verify	0.75	0.89	0.92		0.87	
Psi Blast	6.4e-90	6.4e-91	1.6e-90	1.6e-90	3.2e-91	3.2e-91
END	213	213	213	213	213	213
STAR T AA	52	25	25	25	25	25
CHAI	∢	<	4	<	<	∢
EDB EDB	Iduz	lefx	Ihsa	lhsa	lhsb	lhsb
SEQ No.	1272	1272	1272	1272	1272	1272

PDB annotation	MAJOR IIISTOCOMPATIBILITY COMPLEX MIC ONOCLASSICAL CHAIN, MHC-B, HLA-E, MHC CLASS HLA-E, HLA-E, MADOR HS-E, HLA-E, MADOR HSTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MHC, HLA, 2 BETA 2	CLARDR PEPTIDE, 3NON- CLASSICAL, MHC, CLASS IB MHC CLASSICAL, MHC, CLASS IB MHC COMPLEX WICK ONDICASSICAL COMPLEX WICK ONDICASSICAL HAAE, HAAE, MAGN HAAE, HAAE, MADN MHC, HAA, 28ETA, 2 MHC, HAA, 28ETA, 2 ISAALRA PEPTIDE, 3NON- ISAALRA PEPTIDE, 3NON- ISAALRA PEPTIDE, 3NON- ISAALRA PETIDE, 3NON- ISAALRA PETID	LLASSUCH MHC, CLASS IB MHC, MANUNG SYSTEM IMMUNOGLOBULIN (109-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM		
Coumpound	HIA CLASS I HISTOCOMATIBILITY HISTOCOMATIBILITY ANTIGEN HIA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (WAPRITVLL); CHAIN: P, Q;	HA CLASS I HISTOCOMPATIBILITY ANTICOMPATIBILITY BETA-SANGCOLOBULIN; CRANE, B. PETTIDE (VMARRTVLL); CHAIN: P. Q.	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (FLA). CW4 CHAIN: A; BETA-2 MICROGLOBULN: CIAIN: B; FLA-CW4 SPECIFIC PEPTIDE; CHAIN: C:	HISTOCOMPATIBILITY ATMGEN RUNCATED HUMAN CLASS I HUMAN CLASS I HUMAN CLASS I ANTIGEN HILLTY ANTIGEN HILLAY COMPLEXED WITH A COMPLEXED WITH A ENDOAMBLE PERTIDE ENDOAMBLE PERTIDE ENDOAMBLE PERTIDE ENDOAMBLE PERTIDE	HISTOCOMPATIBILITY ANTIGEN TRUNCATED
SEQFOL D score		144.34			215.19
PMF	1.00		1.00	00.1	
Verify	0.92		0.67	0.83	
Psi Blast	4.8e-87	4.8c-87	86-89	9.66-87	9.6e-87
END	213	213	213	201	205
STAR T AA	26	26	26	25	25
CHAI	<	<	<	<	4
808 CI	Imhe	1mhe	Iqqd	Itmc	Itmc
SEQ NO:	1272	1272	1272	1272	1272

PDB annotation		COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HNY, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEY, COMPLEX (ANTIGEN/PEPTIDE)	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	HISTOCOMPATIBILITY COMPLEX B8: B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	IMMUNOGLOBULIN FOLD	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR,
Coumpound	HUMAN CLASS I HSTOCOMPATBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMENC PEPTIDE (EVAPEFYHK) ITMC 4	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYYLL - INDEX PEPTIDE); CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HLA-A*0201; CHAIN: A, D; BETA-Z MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, E.	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-
SEQFOL D score			221.84		223.96		
PMF		1.00		1.00		1.00	1.00
Verify		0.98		1.14		1.27	1.17
Psi Blast		6.4e-97	6.4e-97	3.2e-97	3.2e-97	1.16-95	4.8e-97
END		205	219	205	219	205	205
STAR T AA		22	St.	25	25	25	25
CHAI N ID		<	V	⋖	∢	⋖	٧
PDB ID		Jaln	lain	lagd	Ingd	Iduz	1efx
SEQ ID NO:		1273	1273	1273	1273	1273	1273

PDB annotation	IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX					MAMUNE SYSTEM IMMUNGOLOBULIN (IG)-LIKE DOMAIN, ALPHA HELLX, BETA SHEET, 2 IMMUNE SYSTEM	
Coumpound	MICROGLOBULIN; CHAIN; B; PETTIDE FROM IMPORTIN ALPHA-2; CHAIN; C; NATURAL KILLER CELL RECEPTOR KIRZDI.2; CHAIN; D, E;	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3/HLA- BASTIERISR\2705\$ 1HSA 4	HISTOCOMPATIBILITY ANTICEN HUMAN CLASS I HISTOCOMPATIBILITY ANTICEN 1HSA 3 /HLA ANTICEN 1HSA 3 /HLA BÓSTFRISK)ZTOSS 1HSA 4	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTICEN A W681 (LEUCOCYTE H8B 3 ANTICEN) HISB 4	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW6.1 (LEUCOCYTE HISB 3 ANTIGEN) HISB 4	HISTOCOMPATIBILITY LEUKOCYTE ANTOEN (HLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	HISTOCOMPATIBILITY
SEQFOL D score			222.04		245.70		
PMF		1.00		0.1		0.00	1.00
Verify		1.12		1.03		1.07	1.25
Psi Blast		I.6e-96	1.6e-96	1.6e-97	1.6e-97	I.1e-95	1.6e-93
END		205	219	205	218	205	199
STAR T AA		25	25	23	25	26	25
CHAI		∢	∀	¥	¥	∢	٧
PDB CI		Ihsa	lhsa	lhsb	lhsb	Iqqd	Itmc
Se o		1273	1273	1273	1273	1273	1273

PDB annotation			GENE REGILATION POZ DOMAIN; PROTEIN-ROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRICTURE, RROWEZLOCTTIC LEUKEMA, GENE REGILLATION	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER ROTELLY, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMEDIO-TIC	
Coumpound	ANTIGEN TRUNCATED HISTOCOMPATIBILITY ANTIGEN HILA-A W68 ITMC3 COMPLEXED WITH A DECAMENIC PEPTIDE (EVAPPETRIC) ITMC4	ANTIGEN TRUNCATED HUMAN CLASS I HUMAN CLASS I HUMAN CLASS I ANTIGEN HLA-AW68 ITMC 3 ONDELENED WITH A DECAMENIC PETIDE (EVAPETRRS) ITMC 4	PROMYELOCYTIC LEIREMIA ZINC RINGER PROTEIN PLZF; CHAIN: A;	PROMYELOCYTIC LEUKEMIA ZINC RINGER PROTEIN PLZP; CHAIN: A;	OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE
SEQFOL D score		273.81			
PMF			1.00	66'0	0.17
Verify			0.30	0.41	0.05
Psi Blast		1.60-93	1.66-22	3.46-28	1.1e-11
END		199	126	128	458
STAR T AA		23		vo	291
CHAI		₹.	∢	∢	
PDB TD		Itmc	1buo	Ibuo	lgof
SEQ ID	Ö	1273	1274	1274	1274

PDB annotation			STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COLLED COLL, CONTRACTILE PROTEIN	TRANSCRIPTION REGULATION	-		RIBOSOME RIBOSOME- INACTIVATING PROTEIN TYPE II	RIBOSOME RIBOSOME- INACTIVATING PROTEIN TYPE II	TRANSFERASE GLYCOSYLTRANSFERASE
Coumpound	(E.C.1.1.3.9) (PH 4.5) 1GOF 3	OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (B.C.1.1.3.9) (PH 4.5) 1GOF 3	ALPHA SPECTRIN; CHAIN: A, B, C;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	RNA POLYMERASE PRIMARY	SIGMA FACTOR; CHAIN: NULL;	COMPLEX (GLYCOSIDASE/CARBOHYDRA (TE) ABRIN-A COMPLEXED WITH TWO SUGAR CHAINS 1ABR 3	RIBOSOME-INACTIVATING PROTEIN TYPE II, CHAIN: A; RIBOSOME-INACTIVATING PROTEIN TYPE II, CHAIN: B	RIBOSOME-INACTIVATING PROTEIN TYPE II, CHAIN: A; RIBOSOME-INACTIVATING PROTEIN TYPE II, CHAIN: B	SPORE COAT POL YSACCHARIDE BIOSYNTHESIS PROTEIN
SEQFOL D score			65.74	59.43	76.16					
PMF		0.13					0.40	0.21	0.13	0.28
Verify		0.27					0.45	0.16	-0.25	60.0
Psi Blast		1.6e-08	6.8e-09	3.40-12	5.1e-05		1.4e-09	1.2e-15	0.00011	6.4e-22
END		495	385	415	416		552	552	543	345
STAR		383	170	. 081	130		413	1441	450	123
CHAI N ID			<	¥.			В	ш	æ	¥
EDB CI		lgof	lcun	Iquu	Isig		labr	1ce7	lce7	lqgq
SEQ No. ID		1274	1275	1275	1275		1276	1276	1276	1276

PDB aunotation		HYDROLASE XYLAN DEGRADATION						IMMUNOGLOBULIN	CATALYTIC ANTIBODY	CATALYTIC ANTIBODY, ESTERASE	CATALYTIC ANTIBODY	CATALYTIC ANTIBODY, ESTERASE	COMPLEX (IMMUNOGLOBULIN/VIRAL	PEPTIDE) ANTIBODY 8F5;	IMMUNOGLOBULIN, ANTIBODY,	RHINOVIRUS, NEUTRALIZATION, 2	CONTINUOUS EPITOPE, COMPLEX	(IMMUNOGLOBULIN/VIRAL	PACIFICAL OPITING	IMMUNOGLOBULIN, ANTIBODY,	CATALYTIC ANTIBODY, DIELS	ALDER, 2 GERMLINE	IMMUNOGLOBULIN	IMMUNOGLOBULIN, FAB,	ANTIBODY, ANTI-E-SELECTIN
Coumpound	CHAIN: A;	ENDO-1,4-BETA-XYLANASE; CHAIN: A, B;	GLYCOSIDASE RICIN (E.C.3.2.2.2) 2AAI 3	TRANSFERASE (PHOSPHOTRANSFERASE)	ADENYLATE KINASE	ISOENZ YME-3 (GTP: AMP PHOSPHOTIR ANSFER ASE) 2AK3	3 (E.C.2.7.4.10) 2AK3 4	2E8 (IGG1=KAPPA=) ANTIRODY: CHAIN: I. H. M. P.	29G11 FAB; CHAIN: L, H;		29G11 FAB; CHAIN: L, H;		IGG2A; CHAIN: L, H; HUMAN RHINOVIRUS CAPSID PROTEIN	VP2; CHAIN: P;					PARTINOGLOBIT BUDIETS	ALDER CATALYTIC	ANTIBODY; CHAIN; L, H, A, B;		MONOCLONAL ANTI-E-	SELECTIN 7A9 ANTIBODY;	CHAIN: L, H;
SEQFOL D score									19.19				60.58										90.19		
PMF		99'0	0.03	86.0				0.21			0.27			_					0.17	1.					
Verify		-0.02	-0.31	-0.87				0.01			-0.31								11.0	į					
Psi Blast		1,6e-16	1.3e-07	1.3e-16				1.3e-38	6.4e-37		6.4e-37		1.3e-36						0 60 27	600			3.2e-35		
END AA		543	543	38				253	254		253		256						250	1			256		
STAR		441	441	_				59	50		59		20	_			_		17	5			48		
CHAI N ID		<	В	<				II.	H		H		н						-	1			н		
PDB		lxyſ	2aai	2ak3				12c8	1a0q		1a0q		la3r						10/1	F			la5f		
SEQ NO:		1276	1276	1279				1280	1280		1280		1280	_					1280	25.	_		1280		

PDB annotation	COMPLEX (INMALINGALDULIN/AUTOANTIGE N) COMPLEX (IMMALINGALDBULINAUTOANTIGE N), REEUMATOID FACTOR 2 AUTO- ANTIBODY COMPLEX ANTIBODY COMPLEX	COMPLEX (VIRAL CAPRIDIAMAUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24, FAB, FAB LIGHT CHAIN, FAB HIRAYY CHAIN COMPLEX (VIRAL CAPRIDIAMAUNOGLOBULIN), HIV, CAPRID PROTEIN, 2 P24	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY FAB', CATALYST, ALDOLASE REACTION	MAUNDE SYSTEM MAUNDE SYSTEM MAUNOGLOBELIN, BYANDAGLOBELIN, BYANDAGLOBELIN, CHIMANAZEDAN CHIMANAZEDAN CHIMANAZEDAN CHIMANAZEDAN CHIMANAZENA SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM	ANTIBODY ENGINEERING ANTIBODY SIGNEERING, HUMANIZED AND CHIMERIC ANTIBODIES, 2 FAB, X-RAY SIRUCTURES, GAMMA-	IMMUNOGLOBULN IMMUNOGLOBULN, KAPPA LIGHT-
Coumpound	IGG4 REA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;	HUMAN IMMUNODEFICIENCY VRUS TYPE I CAPSID CHAIN: A, B, ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	IMMUNOGLOBULIN IGG2A; CHAIN: L, H;	THE THE CHAIN; CHAIN; CHAIN; CHAIN; CHAIN; CHAIN; H; CHAIN; CHAIN; H; CHAIN; CH	ANTIBODY; CHAIN: L, H;	IMMUNOGLOBULIN; CHAIN: A, B;
SEQFOL D score			56.82			
PMF	0.00			-0.07	0.09	0.13
Verify	-0.04	0.08		0.04	0.00	-0.12
Psi Blast	1.1e-37	4.8e-37	4.8e-33	8e-39	1.4e-37	4.8e-37
END	255	253	256	258	258	252
STAR T AA	20	22	15	15	21	51
CHAI N ID	7	н	I	ı	ji	٧
PDB	Iado	1afv	laxt	162w	1b4j	156d
SEQ NO:	1280	1280	1280	1280	1280	1280

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PDB annotation	CHAIN DIMER HEADER	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX	(ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNE	SYSTEM		IMMUNE SYSTEM	IMMUNOGLOBULIN							IMMUNE SYSTEM ANTIBODY (FAB	FRAGMENT), IMMUNE SYSTEM			ANTIBODY THERAPEUTIC, ANTIBODY, CD52			IMMUNE SYSTEM ANTI-PRION FAB	3F4; ANTI-PRION FAB 3F4 ANTI-	PRION ANTIBODY, FAB 3F4		
Coumpound		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR	ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	MONOCLONAL ANTIBODY MRK-16 (LIGHT CHAIN);	CHAIN: A, C; MONOCLONAL ANTIBODY MRK-16 (HEAVY	CHAIN); CHAIN: B, D,	IMMUNOGLOBULIN OPG2 FAB,	CONSTANT DOMAIN; CHAIN:	EAR VARIABLE DOMAIN:	CHAIN: H;	COMPLEX	(ANTIBODY/ANTIGEN) HYHEL-	5 FAB COMPLEXED WITH	BOBWHITE QUAIL LYSOZYME IBOL 3 IBOL 95	ANTIBODY R24 (LIGHT	CHAIN); CHAIN: A; ANTIBODY	R24 (HEAVY CHAIN); CHAIN:	В;	CAMPATH-TH:LIGHT CHAIN; CHAIN: L; CAMPATH-	HHEAVY CHAIN; CHAIN: H;	PEPTIDE ANTIGEN; CHAIN: P;	FAB ANTIBODY LIGHT CHAIN;	CHAIN: L; FAB ANTIBODY	GOMBLEY	(ANTIBODY/ANTIGEN) FAB	FRAGMENT OF THE
SEQFOL D score				57.09			57.73				59.53				57.49									08 95	20:00	
PMF		60.0-																	-0.03			09:0				
Verify		0.09																	11.0			-0.12				
Psi Blast		8e-38		4.8e-35			1.6e-34				3.2e-36				1.6e-26			1	9.6e-37			8e-39		1 60.36	2	
END		252		252		į	258				255				250				727			255		255	ì	
STAR T AA		51		47			51				20				51				10			59		48	-	
CHAI		7		V			н				Ξ				В				_1			Ξ		1	:	
10g E1		16j1		1bln			1bm3				IbdI				1bz7			7	3			lcr9		16.	_	
SEQ NO. B		1280		1280			1280				1280				1280			000.	0871			1280	_	1280		

PDB annotation	31.4	B IMMUNOGLOBULIN L,			CATALYTIC ANTIBODY CATALYTIC ANTIBODY 6D9 CATALYTIC ANTIBODY, ESTER HYDROLYSIS, ESTEROLYTIC, FAB, 2 IMMUNOGLOBULIN	() COMPLEX (MANUNOGLOBULIN F. 1GUI/IGG2A)	fi	AB'
Coumpound	MONOCLONAL ANTIBODY F9.13.7 (IGG1) IFBI 3 COMPLEXED WITH LYSOZYME (E.C.3.2.1.17) IFBI 4	4-4-20 (IG*G2A=KAPPA=) FAB FRAGMENT; IFLR 5 CHAIN: L, H; IFLR 6	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	IMMUNOGLOBULIN 6D9; CHAIN: L, H;	IDIOTYPIC FAB 730.1.4 (1GGI) OF VIRUS 11A1 5 CHAIN: L, H; 11A1 7 ANTI-IDIOTYPIC FAB 409.5.3 (1GG2A); 11A1 9 CHAINI M, 111A1 10	COMPLEX (ANTIBODY/BINDING PROTEIN) IGGI FAB PRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) IIGC 5 PROTEIN G, STREFTOCOCCUS IIGC 15	IMMUNOGLOBULIN IGGI FAB' PRAGMENT (B1312) 11GF 3
SEQFOL D score		56.39		57.20	57.33	60.65	57.26	58.26
PMF			-0.12					
Verify			0.11					
Psi Blast		3.2e-33	1.4e-37	6.4e-32	1.36-34	4.8e-33	1.6e-32	86-35
END		256	258	258	255	254	528	258
STAR T AA		21	51	51	47	48	21	47
CHAI N ID		н	V V	я	<u></u>	H	Ħ	1
EDB TD		1flr	PvJI	Jfvd	Ihyx	liai	ligo	ligf
Se o Se		1280	1280	1280	1280	1280	1280	1280

PDB annotation	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION	CATALYTIC ANTIBODY SULFIDE OXIDATION, MONOOXYGENASE, OXYGENATION, FAB, 2 IMMUNOGLOBULIN, CATALYTIC ANTIBODY		MUSCLE BROTEIN CONNECTIN, NEXTMS; CELL ADHESION, GLYCORKOTEN, TRANSMEMBRANG, REPEAT, BRAIN, 2 IMANINOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 ALTERNATIVE SPLICING, SIGNAL, 3	IMMUNOGLOBULIN IMMUNOGLOBULIN	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGER, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, COMPLEX (ANTIBODY/PEPTIDE EPITOPE)	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY,
Coumpound	IGGI INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	28B4 FAB; CHAIN: L, H;	IMMUNOGLOBULIN FAB D44.1 (IGG1,KAPPA) (BALB/C MOUSE, MONOCLONAL ANTIBODY) IMLB 5	TITIN; CHAIN: NULL;	NIG9 (IGGI=LAMBDA=); CHAIN: L. H:	SM3 ANTIBODY; CHAIN: 1., H; PEPTIDE EPITOPE; CHAIN: P;	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	SM3 ANTIBODY; CHAIN: I, H; PEPTIDE EPITOPE; CHAIN: P;
SEQFOL D score		57.31	56.48			58.83		56.66
PMF	0.37			0.35	0.22		0.41	
Verify	0.02			0.08	-0.09		-0.09	
Psi Blast	1.6e-36	6.4e-34	8e-36	0.0015	6.4e-37	I.6e-36	1.6e-36	3.2e-30
END	253	255	258	254	253	256	253	252
STAR	59	51	84	178	51	51	29	20
CHAI N ID	m	I	8		н	H	н	1
PDB II	ligy	Ikel	lmlb	Inct	Ingp	Ism3	Ism3	lsm3
SEQ NO:	1280	1280	1280	1280	1280	1280	1280	1280

\Box	_				T			T	
PDB annotation		2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)			COMPLEX (ANTIBODY/BLECTRON TRANSORI) PAB ES; CYTC, ANTIGEN; IMMUNOGLOBULIN, IGGI KAPPA, FAB FRAGMENT, HORES 2 CYTOCRROME C, COMPLEX (ANTIBODY/BLECTRON TRANSORY)	TRANSFERASE TRK RECEPTOR, RECEPTOR TYROSINE KINASE, 3D- DOMAIN SWAPPING, 2 TRANSFERASE	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION	-
Coumpound			IMMUNOGLOBULIN IGGI MONOCLONAL FAB FRAGMENT (TE33) COMPLEX WITH CHOLERA ITET 3 TOXIN PEPTIDE 3 (CFP3) ITET 4	MUSCLE PROTEÍN TITÍN MODULE MS (CONNECTIN) ITIMA 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITINM 4 (ITIMA 58	E8 ANTIBODY; CHAIN: I, H; CYTOCHROME C; CHAIN: F;	NT-3 GROWTH FACTOR RECEPTOR TRKC; CHAIN: A;	IGG 5C8; CHAIN: L, H;	IGG 5C8; CHAIN: L, H;	IMMUNOGLOBULIN IGG2B (KAPPA) FAB FRAGMENT COMPLEXED WITH ANTIGEN 2CGR 3 N-(P-CYANOPHENYL)- N-(DIPHENYLLEMETHYL)
SEQFOL	D score		57.32				57.06		57.12
PMF	score			0.05	0.70	0.01		0.53	
Verify	score			-0.05	0.55	91.0		0.11	
Psi Blast			6.4e-36	0.0051	3.2e-37	0.0051	1.16-37	1.10-37	1.6e-31
END	AA_		256	254	253	254	254	253	254
STAR	TAA		48	178	29	164	8	SS	21
CHAI	e v		Ξ		I	<	Œ	Ħ	ш
PDB	9		ltet.	Itmu	Iwej	lwwc	25c8	25c8	2cgr
SEQ	Αÿ		1280	1280	1280	1280	1280	1280	1280

PDB annotation			COMPLEX (RT/DNA/FAB) HIV-1 RT; FAB 28; AIDS, HIV-1, RT, POLYMERASE		TRANSFERASE TRANSFERASE, CREATINE KINASE	TRANSFERASE BB-CK, BRAIN-TYPE CREATTINE KINASE, BRAIN-TYPE CREATURE KINASE, CANCER, CELLULAR ENERGY 2 METABOLISM, GUANIDINO KINASE, NEURODEGENERATIVE DINORDERS	TRANSFERASE (CREATINE KINASE) UMTCK, MA-CK, MTOCHONDRIAL CELLULAR REREGY 2 METABOLISK, GANGER, METABOLISK, GIANIDINO KINASE, MITOCHONDRIAL PERMEABILITY STANNITION, OCTAMBE STANNITION,	TRANSFERASE CREATINE KINASE,
Coumpound	GUANIDINEACETIC ACID 2CGR 4	IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 152' (HUHS2-OZ FAB) 2FGW 4	HIV-I REVERSE TRANSCRIPTASE; CHAIN: A, B; MONOCLONAL ANTIBODY 28; CHAIN: C, D; DNA; CHAIN: E, F;	IMMUNOGLOBULIN IMMUNOGLOBULIN FAB' NEW (LAMBDA LIGHT CHAIN) 7FAB	CREATINE KINASE; CHAIN: A, B, C, D;	CREATINE KINASB, B CHAIN; CHAIN: A, B, C, D;	CREATINE KINASE, UBIQUITOUS MITOCHONDAIAL; CHAIN: A, B, C, D, E, F, G, H;	CREATINE KINASE; CHAIN: A;
SEQFOL D score			56.78	57.01				
PMF		80.0-			0.27	0.30	0.33	0.19
Verify score		0.00	,		-0.83	-0.83	-0.83	-0.83
Psi Blast		1.6e-38	4.8c-33	3.2e-31	3.2e-19	4.86-19	6.4c-19	1.4e-19
END AA		258	258	255	46	46	46	46
STAR T AA		51	47	49	_	-	-	_
CHAI		1	ပ	н	٧	Ą	٧	Ą
PDB ID		2fgw	2hmi	7fab	1crk	1gh4	19,81	2crk
SEQ No:		1280	1280	1280	1284	1284	1284	1284

PDB annotation	TRANSFERASE	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK	ULL; MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE	ULL; MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE	ULL; MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE			CDC42, 2 PHOSPHOINOSITIDE 3-	KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL	TRANSDUCTION	3- PHOSPHOTRANSFERASE RHOGAP DOMAIN: PHOSPHOTE ANSFER A ST	TPASE ACTIVATING PROTEIN GAD	CDC42, 2 PHOSPHOINOSITIDE 3-	KINASE, SH3 DOMAIN, SH2	DOMAIN, 3 SIGNAL	G-PROTEIN CDC42 GTPASE-	ACTIVATING PROTEIN; G-PROTEIN,	
Coumpound		DNAJ; CHAIN: NULL;	DNAJ; CHAIN: NULL;	HUMAN HSP40; CHAIN: NULL;	HUMAN HSP40; CHAIN: NULL;	HUMAN HSP40; CHAIN: NULL;		PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B;				PHOSPHATIDYLINOSITOL 3-	MINASE, CHAIN: A, B,				RHOGAP; CHAIN: NULL;		P50-RHOGAP; CHAIN: A;
SEQFOL D score			68.92		83.03			93.22				94.15					109.76		114.46
PMF		1.00		1.00		1.00													
Verify score		0.89		0.77		1.26													
Psi Blast		1.1e-27	1.1e-27	3.4e-30	3.4e-30	1.6e-27		6.4e-08				8e-09					4.8e-17		1.1e-17
END		69	78	77	80	69		300				314					288		302
STAR T AA		10	5 0	10	5	7	į	112				112					66		105
CHAI N ID							ĺ	¥				m							<
PDB UI		1bq0	1bq0	1hdj	[þ4I	Ihdj		lpbw				Ipbw					Irgo		1tx4
SEQ NO:		1287	1287	1287	1287	1287		1292				1292					1292		1292

PDB annotation	GTPÁSE-ACTIVATING PROTEIN RHOGAP, COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP	COMPLEX COMPLE		METALLOPROTEINASE MATRIX METALLOPROTEINASE-3; MATRIX METALLOPROTEINASE, MMP-3, NON-PEPTIDE INHIBITOR	HYDROLASE MMP-2,72KD TYPE IV COLLAGENASE; HYDROLASE (MGTALLOPROTEASE), FULL- LENGTH, METALLOPROTEINASE, 2 GELATINASE A	HYDROLASE COL-2; BETA SHEET, ALPHA HELIX, HYDROLASE	METALLOPROTEASE
Coumpound	RHOA; CHAIN: B;	MEDALOPROTENASE, METALOPROTENASE, CHAPI, M; METALOPROTENASE METALOPROTENASE PHEBITOR, CHAPI: T;	HYDROLASE (METALLOPROTEASE) COLLAGENASE (E.C.3.4.24.7) (CATALYTIC DOMAIN) CRYSTAL FORM 11CGE 3	STROMELYSIN-1; CHAIN: A;	GELATINASE A; CHAIN: A;	HUMAN MATRIX METALLOPROTEINASE 2; CHAIN: A;	FIBROBLAST (INTERSTITIAL)
SEQFOL D score		103.34	120.96	132.96	647.13	90.80	151.00
PMF							
Verify score							
Psi Blast		9.6e-54	8-60	4.8e-63	0	9.6e-14	3.2e-70
END		281	254	272	669	333	449
STAR		1112	110	107	25	274	107
CHAI N ID		M		∢	¥	<	
PDB ID		1bqq	1cge	lciz	10k7	Icxw	1491
SEQ No.		1293	1293	1293	1293	1293	1293

PDB annotation		HYDROLASE (METALLOPROTEASE) MMP-2, 7120 TYPE IV COLLAGENASE, HYDROLASE, HEMOPEXIN DOMAIN, HYDROLASE, METALLOPROTEASE	i.	1, MATRIN; IMMQ 7	METALLOPROTEASE MMP-13; C- TERMINAL HEMOPEXIN-LICE DOMAIN OF MATRIX- METALLOPROTEINASE	HYDROLASS MATRIX HETALLOPROTEINASE2; INHIBITOR, MATRIXIM, MATRIX METALLOPROTEINASE2; (MMP-2), 2 GELATINASE4, METZINCIN, HYDROLASE	HYDROLASE MATRIX METALOPROTEINASE-3, PROTEOGLYCANASE; HYDROLASE, METALLOPROTEASE; HEROBLAST, COLLAGEN DEGRADATION	MATRIX METALLOPROTEASE MMP-13: MATRIX METALLOPROTEASE	HYDROLASE MMP-2,72KD TYPE IV COLLAGENASE; HYDROLASE (METALLOPROTEASE), FULL-
Coumpound	COLLAGENASE (MMP-1); 1FBL 4 CHAIN: NULL; 1FBL 5	GELATINASE A; CHAIN: NULL;	METALLOPROTEASE FIBROBLAST COLLAGENASE (E.C.3.4.24.7) 1HFC 3	MATRILYSIN; IMMQ 5 CHAIN: NULL; IMMQ 6	COLLAGENASE-3; CHAIN: NULL;	GELATINASE A; CHAIN: A;	STROMELYSIN-1; CHAIN: NULL;	MMP-13; CHAIN: A, B;	GELATINASE A; CHAIN: A;
SEQFOL D score		99.59	117.07	119.28	84.70	144.06	187.06	138.28	419.38
PMF									
Verify									
Psi Blast		9.6e-50	8e-60	8e-56	4.8e-63	1.6e-57	1.6e-82	1.6e-59	0
END AA		669	265	279	669	272	272	267	432
STAR		474	115	107	477	112	4	107	25
CHAI						∢		4	∢ .
PDB		lgen	Thfe	lmm 9	1pex	1qib	1slm	830c	1ck7
SEQ NO:		1293	1293	1293	1293	1293	1293	1293	1294

PDB annotation	LENGTH, METALLOPROTEINASE, 2 GELATINASE A	HYDROLASE COL-2; BETA SHEET, ALPHA HELIX, HYDROLASE	UBIQUITIN CONUGATION UBC7; UBIQUITIN CONUGATION, LIGASE, YEAST		INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILC ADHESION	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18	COMPLEX (IMMUNOCLOBULIN/RECEPTOR) IMMUNOCLOBULIN/RECEPTOR) IMMUNOCLOBULIN/FOLD, GLYCOROTENI, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOCLOBULIN/RECEPTOR)	TRANSDUCTRONREGULATOR GI- TRANSDUCTRONREGULATOR GI- FROTTRIN SIGNALLING 4; GI-AITHA, I ATDROLANE, SIGNAL I ATDROLANE, SIGNAL I ATDROLANE, SIGNAL I TRANSDUCTRON, SEG4, 2 COMPLEX TRANSDUCTRONREGULATOR), GIENDARIO, SITP-ASE	COMPLEX (SIGNAL
Coumpound		HUMAN MATRIX METALLOPROTEINASE 2; CHAIN: A;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;		HEMOLIN; CHAIN: A, B;	FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	DYTEK LEUKDA: BETA; CHAIN: A; TYPE I INTERLEUKDA: RECEPTOR; CHAIN: B;	GÜANNE NUCLEGTIDE. BINDING PROTEIN GÜ); CHAN: A. D. ROS4; CHAIN: E, H;	GUANINE NUCLEOTIDE-
SEQFOL D score		90.47	80.92		176.45	104.50	104.57	146.45	133.76
PMF				Ì					
Verify score									
Psi Blast		3.2e-21	3.2e-44		8e-44	8e-18	3.2e-18	4.80-48	6.4e-43
END		333	295		1834	2042	1645	172	169
STAR T AA		274	400		1462	0991	1370	45	54
CHAI N ID		Ą			¥		В	ш	Н
PDB		lcxw	2ucz		1bih	Iff	1ltb	lagr	lagr
SEQ NO.		1294	1297		1298	1298	1298	1301	1301

AMENDECTORNEGULATOR) GI- ALPHA-I: REGULATOR OF G- PROTEIN SIGNALLING 4, GIALIPHA- I- TRANSDUCTION, ROS4, Z COMPLEX (SIGNAL TRANSDUCTION, ROS4, Z COMPLEX TRANSDUCTION REGULATOR), ACTIVATING ROTEIN	SIGNALING PROTEIN REGULATION GALPHA NITERACTING PROTEIN; GAIP, RGS, REGULATOR OF G PROTEIN, SIGNALING PROTEIN 2 REGULATION		OXDOREDUCTASE METHYLENETHE METHENYLTHE'THE METHENYLTHE'THE, BETHYCTRONAE, DEHYDROGENAE, CYCLOHYDROGES, FOLAT, CYCLOHYDROCAES, FOLAT, CYCLOHYDROCAES, FILADER	OXIDOREDUCTASE,HYDROLASE FOLATE, DEHYDROGENASE, CYCLCOHYDROLASE, BIFUNCTONAL, 2 CHANNELING, OXIDOREDUCTASE,HYDROLASE	COMPLEY (TB ANSCRIPTION	COMPLEA (IKANOCATI 10) REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (REANSCRIPTION REGII ATTON/DNA), DNA-BINDING
BINDING PROTEIN (GD; CHAIN: A, D; RGS4; CHAIN: E, H;	GAIP (G-ALPHA INTERACTING) PROTEIN; CHAIN: A;		METHYL BUTTETRAHYDROFO LATE DEHYDROGENASE / CHAIN: A, B;	FOLD BIFUNCTIONAL PROTBIN; CHAIN: A;	GA BRIDING BROTTEN AT BHA:	CARIN: 4; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, B;
	121.40		94.97	106.54		
					0.50	
					-0.23	770
	3.2e-46		4.8e-74	8e-77	80-34	
	172		235	235	157	ì
	46		S.	-	18	2
	٧		¥	¥	2	1
	lcmz		1a4i	1b0a	fawe	
	1301		1302	1302	1307	
		Handright Charles, April 172 3.26-46 Historich Charles, April 172 3.26-46 Historich Charles, Charles, Charles, Charles, April 172 3.26-46 Historich Charles, Charles, April 172 3.26-46 Historich Charles,	BINDING PROTEIN GD; CHADR; A, Dr RGS4, GFADR; E, H; A 46 172 3.2c-46 121.40 GAIPE A; CHADR; A;	India A 46 172 3.2e-46 121.40 GAIP (G-ALPHA F. A. B. B. G. B. A. B. B. G. B. B. B. B. G. B. B. B. G. B.	121.40 GAIP (G-ALPHA 172 3.2e-46 121.40 GAIP (G-ALPHA 184) A 5 235 4.8e-74 94.97 METHYLENETETRAHYDROFO 184 A 5 235 8e-77 166.54 FOLD BITING TIONAL 196.54 FOLD BITING TIONAL 196.54 PROTENC, CHAIR: A;	Ioniz

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PDB annotation	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAL: COMPLEX	(TRANSCRIPTION REGIL ATTON/DNA) DNA-BINDING	2 NUCLEAR PROTEIN, ETS DOMAIN,	TRANSCRIPTION 3 FACTOR	TUMOR SUPPRESSOR TUMOR	ANKYRIN MOTIF	COMPLEX (KINASE/ANTI-	ONCOGENE) CDK6; P16INK4A,	KINASE, CYCLIN DEPENDENT	KINASE INHIBITORY 2 PROTEIN,	CDK, NK4, CELL CYCLE, MULTIPLE	TUMOR SUPPRESSOR, 3 MTS1,	COMPLEX (KINASE/ANTI- ONCOGENE) HEADER	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	MINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITION PROTEIN/KINASE)	COMPLEX (INHIBITIOR	PROJEIN/KINASE) INHIBITOR	KINASP CELL CVCI E 2 CONTROL	ALPHA/BETA, COMPLEX
Coumpound		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1: CHAIN: B:	DNA; CHAIN: D, E;			P19INK4D CDK4/6 INHIBITOR;	CIMEN: NOLE,	CYCLIN-DEPENDENT KINASE	9; CHAIN: A; MULLIPLE TIMOR SUPPRESSOR: CHAIN:	B;					CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	ží.				CYCLIN-DEPENDENT KINASE	6; CHAIN: A; PISINK4D; CHAIN:	á	
SEQFOL D score																								
PMF		0.29				0.19		0.04							0.00						0.37			
Verify		-0.09				-0.01		0.14							-0.17						0,0			
Psi Blast		4.8e-29				8e-27		6.4e-17							6.4e-26						1.36-23			
END AA		125				160		260							160			_		5	281			
STAR T AA		en .				21		443							21					5	2			
CHAI N ID		æ			Ī			В							В					-	ži.			
e B		lawc				1bd8		1bi7		-					Iblx					18.6	XIQI			
SEQ NO:		1307				1307		1307							1307			_		1000	130/			

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PDB annotation	(INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	CELL CYCLE INHIBITOR P18- INK4C(INK6), CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR	CELL CYCLE INHIBITOR P18- INK4C(INK6), CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	EXTRACELLUI-AR MODULE TUMOR-ASSOCIATED ANTIGEN SOC; EXTRACELLUI-AR MODULE, SCAPENGER RECEPTOR, TUMOUR- ASSOCIATED 2 ANTIGEN, EXTRACELLUI-AR MATIRIX, ELYCOSTLATED PROTEIN	OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALK ALODD BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN
Coumpound		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INFIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	MYOTROPHIN; CHAIN: NULL	MAC2 BINDING PROTEIN; CHAIN: NULL;	TROPINONE REDUCTASE-I; CHAIN: A, B;
SEQFOL D score							112.99	73.73
PMF		0.15	90:0	0.10	0.37	0.01		
Verify		-0.12	0.14	-0.12	0.01	0.14		
Psi Blast		6.4e-25	1.6e-17	1.3e-25	3.2e-24	1.6e-20	1.1e-44	1.6c-66
END		130	292	161	129	127	138	304
STAR T AA			443	18	_	19	26	34
CHAI		¥	<	4	<			V
PDB		1bu9	1d9s	1ihb	lik	Imyo	1by2	Isel
S e S		1307	1307	1307	1307	1307	1314	1315

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PDB annotation	DEHYDROGENASE	OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE	ALKALOID BIOSYNTHESIS,	REDUCTION OF 2 TROPINONE TO	TROPINE, SHORT-CHAIN	OXIDOREDITCTASE NAD.	DEPENDENT OXIDOREDUCTASE.	SHORT-CHAIN ALCOHOL 2	DEHYDROGENASE, PCB	DEGRADATION	OXIDOREDUCTASE SHORT-CHAIN	DEHYDROGENASE,	OXIDOREDUCIASE	DEHYDROGENASE	DEHYDROGENASE, 17-BETA-	HYDROXYSTEROID	OXIDOREDUCTASE SHORT-CHAIN	DEHYDROGENASE/REDUCTASE,	DILE ACID CATABOLISM						OXIDOREDUCTASE SEPIAPTERIN	REDUCTASE,	TETRAHYDROBIOPTERIN,	OXIDOREDUCTASE	OXIDOREDUCTASE NAPHTHOL REDUCTASE: OXIDOREDUCTASE	Control of the contro
Coumpound		TROPINONE REDUCTASE-1; CHAIN: A, B;				CIS-RIPHENVI 23	DIHYDRODIOL-23-	DEHYDROGENASE; CHAIN:	NULL;		CARBONYL REDUCTASE;	CHAIN: A, B, C, D;		17-BETA-HYDROXYSTEROID-	DEHYDROGENASE; CHAIN:	NULL;	7 ALPHA-HYDROXYSTEROID	DEHYDROGENASE; CHAIN: A,	OVIDOPEDITOTASE 2. AT BEA	CONTROLLED COLUMN STREET STREET	DEHYDROGENASE	(FC11153) THDC3	COMPLEXED WITH	CARBENOXOLONE 1HDC 4	SEPIAPTER IN REDUCTASE;	CHAIN: NULL;			TRIHYDROXYNAPHTHALENE REDUCTASE: CHAIN: A. B:	The control of the co
SEQFOL D score		76.92				65 57					69.13			79.80			82.26		74.87	70.1					65.22				82.44	20 00
PMF																														
Verify																														
Psi Blast		9.6e-68				1.66-47	:				3.2e-54			4.8e-32			6.4e-66		4 80.67						3.2e-21				3.2e-61	9 Fee-65
END		304				314	:				297			319			298		306	3					297				308	166
STAR T AA		34				33					35			38			30		ž	3					35				75	32
CHAI		В									A						٧		A	:									∢	<
908 ED ED		lael				1hdb					lcyd			tds			Ifmc		The						loga				lybv	2ae2
SEQ No no SE		1315				1315					1315			1315			1315		1315						1315				1315	1315

Š e Š	EDB CII	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
									CHAIN: A, B;	OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO PSEUDOTROPINE, SHORT-CHAIN DEHYDROGENASE
1321	lpbk		224	339	1.3e-24			194.11	FKBP25; CHAIN: NULL;	ISOMERASE FKBP25 C-TERMINAL DOMAIN; FKBP12 HOMOLOGOUS DOMAIN OF HFKBP25, ISOMERASE
1323	lam4	Ω	31	218	3.26-43			50.20	P50-RHOGAP; CHAIN: A, B, C, CDC42HS; CHAIN: D, E, F;	COMPLEX (GIPASE- ACTIVATING/GIP-BINDING) COMPLEX (GIPASE- ACTIVATING/GIP-BINDING), GIPASE ACTIVATION
1323	1byu	∢.	29	244	3.2e-32			61.74	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1323	Ibyu	m	27	245	4.8e-33			64.26	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1323	lely	<	31	203	4.8e-64			79.57	RAS-RELATED PROTEIN RAP. 14; CHAIN: 4; PROTO- 0NKOGENIE SERINGATHREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1323	1ctq	<	33	204	1.3e-64			93.92	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN, G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1323	lexz	¥	28	204	1.6e-50			52.92	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A: PKN: CHAIN: B:	SIGNALING PROTEIN PROTEIN- PROTEIN COMPLEX, ANTIPARALLEL COLLED-COIL
1323	libr	4	34	500	1.1e-31		П	84.09	RAN; CHAIN: A, C; IMPORTIN	SMALL GTPASE KARYOPHERIN

PDB annotation	BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR	GTP-BINDING PROTEIN GTP- BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY	COMPLEX (SWALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SWALL GTPASE/NUCLEAR PROTEIN),	SMALL GIPASE, 2 NUCLEAR TRANSPORT	COMPLEX (GTP- BINDING/EFFECTOR) RAS-RELATED	PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN,	EFFECTOR, RABCDR, 2 SYNAPTIC	EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	HYDROLASE CDC42/CDC42GAP;	STATE, G-PROTEIN, GAP, CDC42,	ALF3, HYDROLASE	VESICULAR TRAFFICKING GTP	HYDROLYSIS, RAB 2 PROTEIN,	HYDROLASE HYDROLASE	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2
Coumpound	BETA SUBUNIT; CHAIN: B, D;	RAP2A; CHAIN: NULL;	RACI; CHAIN: NULL;	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;				GTP BINDING PROTEIN (G25K);	CHAIN: A; GIFASE ACTIVATING PROTEIN (RHG);	CHAIN: B;	KAB3A; CHAIN: A;			PROTEIN KINASE CK2/ALPHA- SUBUNIT; CHAIN: NULL;
SEQFOL D score		91.54	62.77	59.75		19:69				57.05		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	67.1b			107.93
PMF																
Verify score																
Psi Blast		6.4e-61	1.6e-51	1.1e-31		9.6e-58				1.6e-46		0.0	1.06-58			1.6e-80
END		204	222	227		209				230		,00	504			536
STAR		31	30	31		29				33		95	30			167
CHAI				ပ		¥				٧			۷.			
PDB UD		1kao	1mh1	Irip		1zbd				2ngr		1	Srab			1a6o
SEQ No es		1323	1323	1323		1323				1323		13.53	1323			1324

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PDB annotation	SER/THR KINASE	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAR ROSPORINE, 2 CELL DIVISION, MARCELE DIVISION,	MI COMPLEX (KICHASE/INHIBITOR) CDKG, PIGNIKAD; CYCLIA DEPRIDABIORI KANASE, CYCLIA DEPRIDABIT KITAASE INHIBITORY 2 PROTEIN, CJK, INK4, CELL CYCLE, COMPLEX KITAASE INHIBITOR)	COMPLEX (INHIBITOR PROTEIN/SUNASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHANBETA, COMPLEX (INHIBITOR PROTEIN/KINASE)			PROTEIN KINASE CDK2; TRANSERASE, SERNIFTHEONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORY I, ATTON
Coumpound		CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6: CHAIN: 4, C; CYCLIN- DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	CYCLIN-DEPENDENT KINASE 6, CHAIN: A; PI9INK4D; CHAIN: B;	PHOSPHOTRANSFERASE CAMF-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK 3 (E.C.2.7.1.37) ICMK 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP. DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;
SEQFOL D score		129.21	122.05	133.50	102.25	102.19	141.09
PMF							
Verify							
Psi Blast		0	1.6e-81	3.2e-91	8e-48	3.2e-47	0
END		503	493	499	503	503	503
STAR		196	197	192	160	165	961
CHAI			V	<	9	ш	
PDB CD		laql	1bi8	1bk	lcmk	letp	1bcl
SEQ ID NO:		1324	1324	1324	1324	1324	1324

PDB annotation	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38, PROTEIN SER/THR-KINASE, SERNBÉ/THREONINE-PROTEIN KINASE	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	TRANSFERASE MITOGEN ACTIVATED FROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINETHREONINE-PROTEIN KINASE, 2938	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERNBETHREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHBITION
Coumpound	P38 MAP KINASE; CHAIN: NULL;	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TWITCHIN; CHAIN: A, B;	MAP KINASE P38; CHAIN: NULL;	ERK2; CHAIN: NULL;	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	PROTEIN KINASE CK2/ALPHA- SUBUNIT, CHAIN: NULL;	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;
SEQFOL D score	117.40	136.35	105.97	150.88	128.64	140.27	108.11	129.37
PMF								
Verify								
Psi Blast	1.6e-97	9.6e-100	1.6e-51	0	0	0	6.4e-80	0
END	267	563	522	570	908	509	496	503
STAR	180	180	170	179	190	181	167	961
CHAI N ID			4					
PDB CI	lian	1jnk	lkob	1p38	1pme	3erk	la60	laqı
SEQ No:	1324	1324	1324	1324	1324	1324	1325	1325

PDB annotation	COMPLEX (KINASE/NHIBITOR) CDKG, FIDINGED, CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 RROTFIN, CDK, INK4, CELL, CYCLE, COMPLEX (KINASE/NHIBITOR)	COMPLEX (INHIBITOR PROTEIN/CRIANSE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASK, CELL, CYCLIS, 2 CONTROL, ALPHARBETA, COMPLEX (INHIBITOR PROTEIN/CINASE)			PROTEIN KINASE CDK2; TRANSPERASE, SERINETHEGONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, GELL DIVISION, MITOSIS, PHOSPHORYLATION	SERINETTHREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SERTHR-KINASE, SERINETHREONINE-PROTEIN KINASE	TRANSFERASE JNK3;
	COM CDKC DEPE DEPE COM				PROT TRAD SERII KINA CYCI	SERINE/ KINASE SER/THE SERINE/ KINASE	TRAD
Coumpound	CYCLIN-DEPENDENT KINASB 6(GHAIN) A, GYCLIN- DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; PI9INK4D; CHAIN: B;	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP. DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBINIT) 1CTP 4	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NUILI;	P38 MAP KINASE; CHAIN: NULL;	C-JUN N-TERMINAL KINASE;
SEQFOL D score	122,26	133.76	102.41	102.34	141.19	118.03	136.46
PMF							
Verify							
Psi Blast	8e-86	1.3e-94	3.2e-49	3.2e-49	0	0	4.8e-100
END	493	499	503	503	503	567	563
STAR	197	192	160	591	961	180	180
CHAI N ID	∢	∢	Э	E			
PDB ID	16:8	1blx	1cmk	letp	Ihcl	lian	ljik
SEQ NO: DE	1325	1325	1325	1325	1325	1325	1325

PDB annotation	TRANSFERASE, INK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	TRANSFERASE MITOGEN ACITYA/TED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERNIP/THREONINE-PROTEIN KINASE, 2793	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION	TRANSFERASE MITOGEN ACTIVATED FROTEIN KINASE, MAP 2, ERK2, TRANSFERASE, SERNINE/THREONINE-ROTEIN KINASE, MAP KINASE, 2 ERK2	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE	HYDROLASE PROSEGNIENT, PROPEPTIDE, INHIBITION, HYDROLASE	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS I AND 2, ECADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN,
Coumpound	CHAIN: NULL; T	TWITCHIN; CHAIN: A, B; K	MAP KINASE P38; CHAIN: NULL; T R R R R R	ERK2; CHAIN: NULL; S	TITIN, CHAIN: A, B;	EXTRACELLULAR REGULATED KINASE 2; A CHAIN: NULL; S S	HUMAN PROCATHEPSIN L; F. CHAIN: A; F. F. F.	HUMAN PROCATHEPSIN L; P. CHAIN: A; P. H.	B-CADHERIN; CHAIN: A, B; E
SEQFOL D score		106.60	151.09	128.85	99.53	140.42	368.72	412.39	124.30
PMF									
Verify									
Psi Blast		9.6e-53	0	0	1.1e-44	0	0	0	8e-50
END		522	570	268	615	509	350	391	269
STAR T AA		170	179	190	194	181	-	19	89
CHAI N ID		Ą			¥		V	∢	A
PDB ID		lkob	1p38	Ipme	Itki	3erk	1cs8	lcs8	1edh
S e S		1325	1325	1325	1325	1325	1327	1328	1333

PDB annotation	CELL ADHESION PROTEIN CELL ADHESION PROTEIN									GUANINE NUCLEOTIDE EXCHANGE FACTOR RCCI; GUANINE NUCLEOTIDE EXCHANGE FACTOR,	GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER	EYE LENS PROTEIN EYE LENS PROTEIN	EYE LENS PROTEIN EYE LENS PROTEIN	CRYSTALLIN GAMMA II.	CRYSTALLIN	EYE-LENS PROTEIN EYE-LENS PROTEIN, BETA-CRYSTALLIN B,
Coumpound	N-CADHERIN; CHAIN: A;	LIPID-BINDING PROTEIN ADIPOCYTE LIPID-BINDING	PROTEIN COMPLEXED WITH	1ADL 4	LIPID-BINDING PROTEIN RATTY ACID BINDING	PROTEIN (HUMAN MUSCLE,	M-FABP) COMPLEXED 1HMR 3	ELAIDIC ACID HIMR 4	CELLULAR LIPOPHILIC TRANSPORT PROTEIN P2 MYHLIN PROTEIN (P2) 1PMP 3	REGULATOR OF CHROMOSOME CONDENSATION I; CHAIN: A,	B, C;	GAMMAF CRYSTALLIN; CHAIN: NULL	GAMMAE CRYSTALLIN; CHAIN: A. B	GAMMA B-CRYSTALLIN;	CIPALIN: NOTE,	CIRCULARLY PERMUTED BB2- CRYSTALLIN; CHAIN: A, B;
SEQFOL D score	129.50	158.94			146.24				161.49	141.30		122.87	121.88	125.68		96.08
PMF																
Verify																
Psi Blast	8e-52	9.6e-56			6.4e-58				3.2e-55	1.6e-78		1.4e-61	4.8c-63	3.2e-65		1.6e-39
END	268	133			133				133	409		148	148	148		147
STAR	64	3			3				8	11		_		_		_
CHAI N ID	¥								A	A			٧			<
FDB ID	1ncj	ladi			Ihmr				dwdl	lal2		1a45	1a5d	lam E	1	1bd7
SEQ NO:	1333	1335			1335				1335	1340		1345	1345	1345		1345

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PDB annotation	EYE-LENS PROTEIN, 2 MULTIGENE FAMILY	EYE LENS PROTEIN EYE LENS PROTEIN	COMPLEX (CTP- BINDING/ITAA/ISDUCER) BETA1, TRANSDUCIN BETA SUBJUIT; GAMMA, TRANSDUCIN GAMMA SUBJUIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETBROTRIMBR 2 SIGNAL TRANSDUCTON			IRON STORAGE IRON STORAGE	MEMBRANB ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEARNT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GARBERTAI; COMPLEX (TRANSCREPTION 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKTRIN REPEATS, TRANSCRIPTION 3 PACTOR	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
Coumpound		GAMMA-D CRYSTALLIN; CHAIN: A, B	GT-AIPHAGG-AIPHA CHIMBRA, CHAIN: A; GT- BETA; CHAIN: B; GT-CAMMA; CHAIN: G;	EYE LENS PROTEIN BETA-B2- CRYSTALLIN 2BB2 3		FERRITIN; CHAIN: NULL;	HUMAN BETA2- GLYCOPROTEIN I; CHAIN: A;	SA BINDING PROTEIN AL PHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;
SEQFOL D score		122.84	60.77	99.58		273.99	84.05	64.05	54.79
PMF									
Verify score									
Psi Blast		1.3e-62	9.6e-31	1.6e-47		8e-73	1.6e-11	1.66-39	8e-30
END		148	388	148		177	484	192	191
STAR T AA		-	48	-		9	184	38	61
CHAI N ID		٧	В				<	я	
PDB		lelp	Igot	2pp2		2fha	Iqub	lawc	1bd8
SEQ NO:		1345	1345	1345		1352	1353	1363	1363

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PDB annotation	COMPLEX (INHBITOR PROTEIN/KINASD) INHBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHABETA, COMPLEX (INHBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	CELL CYCLE INHIBITOR P18- INK4C(INK6), CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR. ANK-REPEAT	COMPLEX (TRANSCRIPTION REGANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELLX	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
Coumpound	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; PI9INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B PSOD SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	MYOTROPHIN; CHAIN: NULL	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; F; F;	SYNAPTOTAGMIN III; CHAIN: A;	SYNAPTOTAGMIN III; CHAIN: A;
SEQFOL D score	55.34	54.53	54.88	67.03	53.66	64.27		
PMF							0.1	1.00
Verify							0.64	0.49
Psi Blast	8e-29	1.6e-34	8e-34	4.8e-38	3.2e-25	1.6e-38	8.5e-91	3.2e-46
END AA	165	212	162	307	156	243	415	415
STAR T AA		31	s	73	39	31	143	144
CHAI N ID	В	∢	V.	Q		п	4	A
EDB TD	16lx	1bu9	Tilve	1iku	1myo	Jul Juli	Idqv	Idqv
SEQ No:	1363	1363	1363	1363	1363	1363	1366	1366

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PDB annotation			OXIDOREDITCTASE FATTY ACID	HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK	OXIDOREDUCTASE (OXYGENASE)	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN: NCD CR YSTAI	STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTULE PROTEIN	CONTRACTILE PROTEIN NCD,	CLARET SEGREGATIONAL	PROTEIN; NCD CRYSTAL	MOTORS, KINESIN 2 SUPERFAMILY	CONTRACTILE PROTEIN
Coumpound	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	CYTOCHROWR P450: CHAIN: A		CYTOCHROME P450 ERYF; IOXA 5 CHAIN: NULL IOXA 6	KINESIN; CHAIN: NULL;	KINESIN; CHAIN: NULL;	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D.	î	MICROTUBULE MOTOR	PROTEIN NCD; CHAIN: A, B, C,	ä		
SEQFOL D score		122.64	197.06		67.59	210.20				Ì				
PMF	1.00						1.00	00'1		1.00				
Verify	0.40				-		0.54	0.65		0.46				
Psi Blast	3.4e-40	3.4e-40	1 66-92		3.2e-31	889	889	6.8e-79		3.2c-72				
END	270	270	505		504	340	340	340		341				
STAR	134	134	42		23	2	4	_		_				
CHAI N ID			V					¥		¥				
PDB ID	Irsy	lrsy	Thu7		loxa	ibg2	1bg2	lcz7		1cz1				
SEQ OS SO:	1366	1366	1368		1368	1372	1372	1372		1372				

PDB annotation	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL, PROTEIN, NCD CRYSTAL STRUCTURE, MICROTUBLLE MOTORS, KINESIN 2 SUPERPAMILY,	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD. CONTRACTILE PROTEIN	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD. CONTRACTILE PROTEIN	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED ROTTEIN, MOTOR 2 PROTEIN, ATPASE, P. LOOP, MICROTUBULE BINDING PROTEIN	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P. LOOP, MICROTUBULE BINDING PROTEIN				
Coumpound	MICROTUBULB MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	KINESIN; CHAIN: A, B;	KINESIN MOTOR NCD; CHAIN: A;	KINESIN MOTOR NCD; CHAIN: A;	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;				
SEQFOL D score	156.19	139.58						152.53	185.05	
PMF	В		1.00	1.00	96'0	0.99	1.00			1.00
Verify score			0.25	0.29	-0.01	-0.02	0.46			0.31
Psi Blast	6.8e-79	1.2e-58	3.2c-57	1.2e-58	3.4e-28	8e-27	1.6e-72	1.6e-72	5.1e-74	6.4e-72
END	342	252	252	252	352	358	339	340	338	339
STAR	_	2	4	9	265	265		_	S	9
CHAI N ID	∢	4	4	V	щ	Д	¥	4		
E G	lcz/	2kin	2kin	2kin	2kin	2kin	2ncd	2ncd	3kar	3kar
SEQ NO ID	1372	1372	1372	1372	1372	13.72	13.72	1372	1372	1372

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PDB annotation	CONTRACTILE PROTEIN, KAR3, CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P. LLOOP, MICROTUBULE BINDING PROTEIN	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	COMPLEX (INHIBITOR NITCLE 4 SE)	COMPLEX (INHIBITORNUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION,	EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE).	COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION.	BPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE)	COMPLEX (RI-ANG), HYDROLASE 2	MOLECULAR RECOGNITION,	EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE)	COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (REANG), HYDROLASE?	MOLECULAR RECOGNITION,
Coumpound	KINESIN-LIKE PROTEIN KAR3; CHAIN: NÜLL;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	RIBONITCI BASE INHIBITOR:	CHAIN: B, B; ANGIOGENIN;		RIBONUCLEASE INFIBITOR; CHAIN: A. D. ANGIOGENIN:	CHAIN: B, E;		RIBONUCLEASE INHIBITOR;	CHAIN: B, E;			RIBONUCLEASE INHIBITOR;	CHAIN: A, D; ANGIOGENIN; CHAIN: B. E:	
SEQFOL D score																
PMF	00'1	66'0	86.0	0.04	}		-0.05			0.00				0.37		
Verify	0.50	0.19	-0.10	0.10			0.26			0.10				0.29		
Psi Blast	5.1e-74	1.4e-26	3.2e-26	4.86-17			4.8e-09			9.6e-14				Ie-19		
END	338	352	384	448			545			361				230		
STAR	7	569	269	123			134			45				63		
CHAI N ID		В	В	A	:		¥			V				Ą		
EDB CI	3kar	3kin	3kin	1940	ì		la4y			Ia4y				1a4y		
SEQ El Sign	1372	1372	1372	1373			1373			1373				1373		

PDB annotation	3 REPEATS	COMPLEX (NUCLEAR PROTEINRINA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SYRRYP, RIBONUCLEOPROTEIN		-	PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONLICLEOPROTEIN	-	_	(NUCLEAR PROTEIN/RNA), RNA,	H	_	CNUCLEAR PROTEIN/RNA), RNA,	+		PROIDINKINA) COMPLEA	SNRNP.RIBONUCLEOPROTEIN	INSECT IMMUNITY INSECT	IMMUNITY, LPS-BINDING,	HOMOPHILIC ADHESTON	INSECT IMMUNITY INSECT	IMMUNITY, LPS-BINDING,	HOMOPHILIC ADHESION	CONNECTIN A71, CONNECTIN;	TITIN, CONNECTIN, FIBRONECTIN
Coumpound		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q,	R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q.	R; U2 A'; CHAIN: A, C; U2 B";	CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: O.	R; U2 A'; CHAIN: A, C; U2 B";	CHAIN: B, D;	Tip pale trainment inf. Criticis.	D. IIS 41. OHARE 4 OF TRAIL	K; UZA; CHAIN: A, C; UZB;	Chain; B, D;	HEMOLIN; CHAIN: A, B;			HEMOLIN; CHAIN: A, B;			TITIN; CHAIN: NULL;	
SEQFOL D score																							
PMF		0.42	0.17	0.65		0.53			0.04			220	0.33			0.77			0.25			0.07	
Verify		99.0	0.43	0.55		0.48			0.24			22.0	00:0			0.33			0.37			-0.04	
Psi Blast		5.1e-19	3.4c-22	3.4e-19		3.4e-18			1.4e-22			2 45 10	5.46-19			6.8e-14			1.7e-10			3.40-07	
END		264	220	231		264			220			221	157			387			427			206	
STAR T AA		114	65	06		114			59			8	2			294			295			421	
CHAI N ID		¥	V V	V		S			c			,				A			٧				
PDB ID		la9n	la9n	la9n		la9n			1a9n			1000	TG2I			19ih			Ibih			lbpv	
SEQ NO:		1373	1373	1373		1373			1373			1272	C/CT			1373			1373			1373	

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PDB annotation	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL ADHESION	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL TRANSPILCTION 2 DIMERIZATION	GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH FACTOR RECEPTOR	CELL ADHESION LEUCINE RICH	REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH	REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH	REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH	REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH	REPEAT, CALCIUM BINDING, CELL	ADHESION	TRANSFERASE CRYSTAL	SIRUCIURE, RAIS GERANYLGERANYLTRANSFERASE,
Coumpound	AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	C, D,	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;	INTERNALIN B; CHAIN: A;		INTERNALIN B; CHAIN: A;			RAB	RASE ALPHA SUBUNIT,						
SEQFOL D score																						
PMF	-0.05	61.0	1.00			0.57				0.05		-0.15		0.57		-0.19		0.30			0.23	
Verify	10.0	0.31	9.02			0.29				0.02		60'0		0.13		0.05		0.31			-0.43	
Psi Blast	8.5e-15	3.4e-12	8.5e-14			1.2e-14				6.4e-26		8e-24		1.4e-22		1.6e-14		8e-22			9.6e-09	
END	388	409	389			383				310		332		211		547		265			£	
STAR T AA	286	295	306			296				152		176		37		423		79		:	32	
CHAI N ID	٧	4	υ υ			Д				4		٧		٧		4		Ą			٧	
en En	1cs6	1cs6	lcvs			lcvs				qop1		1d0b		140b		qopi		140b			Idce	
SEQ NO:	1373	1373	1373			1373				1373		1373		1373		1373		1373		9	1373	

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PDB annotation	2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	TRANSFERASE CRYSTAL STRUCTURE, KAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	GROWTH FACTOR/GROWTH PACTOR REGET/OR FGEZ, FGRZ, IMMUNOGI,OBULIN (IG)LIKE DOMAINS BELONGING TO THE I. SET 2 SUBRROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLID	GROWTH FACTOR/GROWTH PACTOR RECEPTOR FGPR2, FGPR2, IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBROUP WITHIN IG-LIKE DOMAINS, B-TREPOIL FOLD	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45, CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, I.RR, LEUCINE- RICH REBEAT, SCF, UBRQUITIN, 2 P3 IRROHITIN, 2	TOTAL PROPERTY AND ADDRESS OF THE PARTY OF T
Coumpound	CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B. D:	RAB GERANYLGERANYLTRANSFE TASE ALPHA SUBUNIT; CHAIN: A, C: RAB GERANYLTRANSFE RASE BETA SUBUNIT; CHAIN; RASE BETA SUBUNIT; CHAIN;	OUTER ARM DYNEIN; CHAIN: A;	FIBROBLAST GROWTH FACTOR 2: CHAIN, A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2: CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN; A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN; B, F, G, H;	SKP2, CHAIN: A, C, E, G, I, K, M, O; SKP1, CHAIN: B, D, F, H, J, L, N, P.	Course out to the course
SEQFOL D score							
PMF		0.15	0.28	80.0-	0.13	0.54	
Verify score		-0.03	-0.41	0.13	0.22	0.26	000
Psi Blast		80-08	1.66-10	5.1e-14	6.8e-16	1.7e-13	2 4- 10
END		171	186	383	387	231	22.1
STAR T AA		37	26	292	296	<u> 2</u>	52
CHAI N ID		<	4	m	Ð	∢	
PDB CI		ldoe	1489	lev2	lev2	Ifqv	160
SEQ El	Š	1373	1373	1373	13.73	1373	1373

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PDB annotation	ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE		MUSCLE PROTEIN CONNECTIN, NEXTMAS, CELL ADHESION, GLYCODROTEIN TRANSMEMBRANE, REPEAT, BRANI, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUNICLE PROTEIN			CELL ADHESION PROTEIN VCAM- D1,2; IVCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING IVCA 15	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, ITRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHSM	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN
Coumpound	CHAIN: B, D;	T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (HUMAN) 1HNF 3	TITIN; CHAIN: NULL;	MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN) ITMM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITMM 4 ITMM 58	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) ITTF 3	HUMAN VASCULAR CELL ADHESION MOLECULE-1; 1VCA 4 CHAIN: A, B; 1VCA 5	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GTPASE-ACTIVATING PROTEIN RNA1 SCHPO;
SEQFOL D seore								
PMF		0.27	0.31	0.76	0.40	0.16	0.00	-0.14
Verify		65.0	0.56	0.60	-0.29	0.46	0.37	0.04
Psi Blast		1.7e-08	6.8e-19	1.7e-16	3.4e-07	1.7e-11	3.4e-12	1.1e-09
END		405	383	383	502	394	411	362
STAR T AA		303	292	305	424	297	280	132
CHAI N ID						Ą	¥	٧
PDB		lhaf	Inct	Itnm	Jm1	Ivca	lwio	lyrg
SEQ NO:		1373	1373	1373	1373	1373	1373	1373

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PDB annotation	FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RANIJP, RANGAP, LERR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMHEIDERAL TWINNING, MEROHEIDRAL TWINNING,	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	IMMUNE SYSTEM PS8 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN	CELL ADHESION PROTEIN NCAM MODULE 2, CELL ADHESION, GLYCOPROTEIN, HEPARIN- BINDING, GPI-ANGELOLE, 2 NEURAL ADHESION MOLECULE, IMMINGGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINEER REGION, 2.2 TANDEM, 3-HELIX COLED-COLLS, STRUCTURAL PROTEIN
Coumpound	CHAIN: A, B;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	MHC CLASS INK CELL RECEPTOR PRECURSOR; CHAIN: A;	NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score						61.31
PMF		0.03	90:00	-0.05	0.35	
Verify score		0.04	0.13	0.20	0.92	
Psi Blast		1.4e-18	1.7e-23	3.46-11	3.4e-17	0.0017
END		359	231	396	383	293
STAR T AA		\$	47	294	296	59
CHAI				¥	<	<
PDB CI		2bnh	2bnh	2dli	3ncm	1cm
SEQ O O		1373	1373	1373	1373	1374

PDB annotation	CONTRACTILE PROTEIN NCD, CLARET SERGREGATIONAL PROTEIN, NCD CRYSTAL STRUCTURE, MICROTUBULE STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P- LLOOP, MCROTUBULE BINDING PROTEIN	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN I, MAJOR BLOOD-STAGE EGF-I IKF DOMAIN
PI	CONTRACTILE PROTEIN CLARET SEGREGATIONA PROTEIN; NOD CRYSTAL STRUCTURE, MICROTUB MOTORS, KINESIN 2 SUP CONTRACTILE PROTEIN	CONTRACTILE PROTEIN HELIX COILED COIL, CONTRACTILE PROTEIN	TRANSCRIPTIC SIGMA70; RNA SIGMA FACTO REGULATION	MOTOR PROTEIN CYTOSKELETON	CYTOSKELETON	MOTOR PROTEIN CYTOSKELETON	CONTRACTILE PROTEIN CONTRACTILE PROTEIN KINESIN-RELATED PROT MOTOR 2 PROTEIN, ATP LOOP, MICROTUBULE BI PROTEIN	MOTOR PROTEIN CYTOSKELETON	MOTOR PROTEIN CYTOSKELETON	SURFACE PR SURFACE AN BLOOD-STAC
Coumpound	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	KINESIN; CHAIN: A, B;	KINESIN; CITAIN: A, B;	KINESIN; CHAIN: A, B;	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	KINESIN HEAVY CHAIN; CHAIN; A. B. C. D.	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MEROZOITE SURFACE PROTEIN I; CHAIN: A;
SEQFOL D score		66.44	65.31			65.43			68.48	
PMF	0.66			0.12	0.81		09.0	98.0		0.03
Verify	-0.46			-0.55	-0.41		-0.52	-0.15		-0.02
Psi Blast	5.1e-34	3.4e-05	0.0017	5.16-15	1.7e-27	1.7e-27	Ie-30	6.8e-25	6.8e-25	5.Ie-19
END	131	295	318	42	141	154	127	142	176	405
STAR T AA	-	53	36	-	55	55	-	59	59	323
CHAI	¥	4		A	В	В		В	m	٧
204 104 104 104 104 104 104 104 104 104 1	lcz/	Idun	Isig	2kin	2kin	2kin	3kar	3kin	3kin	lcej
SEQ NO:	1374	1374	1374	1374	1374	1374	1374	1374	1374	1376

PDB annotation	PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN	SURFACE PROTEIN MEROZOITE	BLOOD-STAGE EGF-LIKE DOMAIN,	EXTRACELLULAR, MODULAR	MALARIA VACCINE COMPONENT,	SURFACE PROTEIN MEROZOITE	SURFACE ANTIGEN 1, MAJOR	BLOOD-STAGE EGF-LIKE DOMAIN,	EXTRACELLULAR, MODULAR	PROTEIN, SURFACE 2 ANTIGEN,	MALARIA VACCINE COMPONENT,	SURFACE PROTEIN	SURFACE PROTEIN MEROZOITE	SURFACE ANTIGEN I, MAJOR	BLOOD-STAGE EGF-LIKE DOMAIN,	EXTRACELLULAR, MODULAR	PROTEIN, SURFACE 2 ANTIGEN,	MALARIA VACCINE COMPONENT,	SURFACE PROTEIN	APOPTOSIS TRAIL; DR5; LIGAND-	RECEPTOR COMPLEX, TRIMERIC	JELLY-ROLL, TNF-R 2	SUPERFAMILY, APOPTOSIS	MEMBRANE PROTEIN NMR,	THROMBIN, EGF MODULE,	ANTICOAGULANT,	TATION	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE,
	PROTEIN, MALARIA SURFACE	SURFACE	BLOOD-S	BXTRACE	MALARIA	SURFACE	SURFACE	BLOOD-S	EXTRACE	PROTEIN,	MALARIA	SURFACE	SURFACE	SURFACE	BLOOD-S	EXTRACE	PROTEIN,	MALARIA	SURFACE	APOPTOS	RECEPTO	DELLY-RO	SUPERFA	MEMBRA	THROMBI	ANTICOA	GLYCOSYLATION	MEMBRA
Coumpound		MEROZOITE SURFACE	(1			MEROZOITE SURFACE	PROTEIN 1; CHAIN: A;						MEROZOITE SURFACE	PROTEIN I; CHAIN: A;						TNF-RELATED APOPTOSIS	INDUCING LIGAND; CHAIN: B;	DEATH RECEPTOR 5; CHAIN:	A;	THROMBOMODULIN; CHAIN:	, Y:			THROMBOMODULIN; CHAIN: A;
SEQFOL D score																												
PMF		0.41				-0.14							0.53							-0.13				0.78				0.15
Verify		-0.11				80.0							60.0							0.30				92.0				0.30
Psi Blast		6.8e-17				5.1e-09							5.1e-21							1.4e-08				5.1e-14				5.1e-18
END AA		435				481							128							733				252				406
STAR T AA		364				403							45							631				181				321
CHAI		A				A							Ą							Ą				Ą				٧
PDB ID		Icej				Icei							Icej							ld4v				1dqb				Idqb
SEQ No.		1376				1376							1376						- The State of the Local Division in the Loc	1376				1376				1376

PDB annotation	ANTICOAGULANT, GLYCOSYLATION	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION	MEMBRANE PROTEIN NMR, THROMBIN, BOF MODULE, ANTICOAGULANT, GLYCOSYLATION	COAGULATION PACTOR CRYSTAL STRUCTURE, EPIDERAAL GROWTH FACTOR, EGF. 2 CALCUUM. BINDING, EGFLICE DOMAN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX.	BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE DOMAIN, BLOOD 2 CLOTTING	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX,
Coumpound		THROMBOMODULIN; CHAIN: A;	THROMBOMODULIN; CHAIN: A;	FACTOR IX; CHAIN: B, C;	BLOOD COAGULATION FACTOR VII; CHAIN: A;	COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	COAGULATION FACTOR XA; CHAIN: A; COAGULATION
SEQFOL D score									
PMF		0.00	0.21	0.23	0.04	0.23	0.42	0.25	0.94
Verify		-0.07	0.25	-0.14	60'0	0.66	0.27	-0.13	80.0
Psi Blast		5.1e-10	5.1e-18	3.4e-07	5.1e-07	1.20-12	3.46-20	1.7e-17	1.4e-15
END		485	131	433	433	254	335	374	445
STAR T AA		400	44	403	403	216	284	327	407
CHAI N ID		∢	∢	д	Ą	ı	T	.1	r
PDB		1dqb	ldqb	ledm	if7e	1fjs	1fjs	Ifjs	1tjs
SEQ NO:		1376	1376	1376	1376	1376	1376	1376	1376

PDB annotation	COAGULATION COFACTOR, PROTEASE	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE					COMPLEX (PROTEASE/INHIBITOR) TYAP, GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)	COMPLEX (PROTEASE/INHIBITOR) TRTAP; GIXTOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)	COMPLEX (PROTEASE/INHIBITOR) TYTAP, GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COGULATION, 2 COMPLEX PROTEASE, PROTEASE, PROTEASE, PROTEASE, PROTEASE, PROTEASE, PROTEASE, PROTEASE/INHIBITOR)	GLYCOPROTEIN GLYCOPROTEIN
	COAGULAT PROTEASE	BLOOD CLO INFIBITOR COAGULAT PROTEASE					COMPLI RTAP; C PROTE/ COAGU	COMPL) RTAP; G PROTE/ COAGU	COMPLI RTAP; C PROTEA COAGU	GLYCO
Coumpound	FACTOR XA; CHAIN: L;	COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	COAGULATION FACTOR BLOOD COAGULATION FACTOR XA 1HCG 3	COAGULATION FACTOR BLOOD COAGULATION FACTOR XA IHCG 3	COAGULATION FACTOR BLOOD COAGULATION FACTOR XA 1HCG 3	COAGULATION FACTOR BLOOD COAGULATION FACTOR XA 1HCG 3	FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	FACTOR XA, CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	FACTOR XA, CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	LAMININ; CHAIN: NULL;
SEQFOL D score										
PMF		0.59	0.46	0.33	68:0	0.95	0.31	0.82	0.34	-0.11
Verify		0.83	0.50	0.34	0.45	0.45	0.01	-0.06	0.66	0.47
Psi Blast		1.7e-12	3.4e-12	1.2e-18	8.5e-15	5.1e-12	3.4e-18	6.8e-15	5.1e-12	6.8e-14
END		8	254	334	445	06	374	445	8	322
STAR		49	217	286	407	49	327	407	49	135
CHAI		ı	В	В	В	В	Т	П	7	
PDB TD		Ifjs	Theg	Theg	Theg	Ihcg	1kig	ıkig	IMg	1klo
SEQ No. to		1376	1376	1376	1376	1376	1376	1376	1376	1376

PDB annotation	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	COMPLEX (BLOOD) COAGULA TION/INHIBITION) COAGULA TION/INHIBITION) CHRISTIMAS I SACTOR; COMPLEX, INHIBITION, HEMCORILLAGOR; BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCUIM, BINDING, HYDROLASE, 3	COMPIEX (BLOOD) COAGULATION/BHIBTOR) COAGULATION/BHIBTOR) CHRISTMAS PACTOR; COMPIEX, INHIBTOR; HEMOTHILA/BGF, BLOOD COAGULATION; 2 PLASMA, SERINE PROTEASE, CALCINI- BINDING, HYDROLA/SE, 3	COMPLEX (BLOOD) COAGULATION/BHIBITOR) COAGULATION/BHIBITOR) COAGULATION/BHIBITOR) INHIBITOR, HANGWIELLA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCUM- BIQUING, HYDROLASE,	SERINE PROTEASE FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE
Coumpound	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	PACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;	FACTOR IXA; CHAIN: C, L.; D. PHE-PRO-ARG; CHAIN: I;	FACTOR IXA; CHAÎN: C, L.; D- PHE-PRO-ARG; CHAÎN: I;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPHTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L;
SEQFOL D score							
PMF	-0.18	0.00	10:0	0.23	0.89	0.37	0.72
Verify score	0.16	0.38	0.04	0.02	0.21	0.28	0.I8
Psi Blast	I.7e-20	8.5e-10	1.7e-14	3.46-27	8.5c-26	I.4e-22	8.5e-16
END	433	787	254	427	152	226	252
STAR T AA	286	979	121	586	14	131	171
CHAI			ы	L)	ப	1	L
90g E1	1klo	1klo	Ağdı T	ZJd1	Ipfx	1qfk	lqfk
SEQ	NO:		1376	1376	1376	1376	1376

PDB annotation	PROTEASE	SERINE PROTEASE FVIIA, FVIIA, BLOOD COAGULATION, SERINE PROTEASE	SERUN PROTEASE FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERIND PROTEASE FVIIA, FVIIA, BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA, FVIIA, BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA, FVIIA, BLOOD COAGULATION, SERINE PROTEASE
Coumpound	COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION PACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C.	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIEBTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPETIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION PACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEFILDYL INHIBITOR; CHAIN: C;
SEQFOL D score						
PMF		0.22	0.29	0.99	0.92	0.52
Verify score		-0.11	-0.01	0.22	0.12	-0.29
Psi Blast		3.4e-26	1.5e-21	16-18	1.7e-24	6.8e-23
END		389	419	445	141	189
STAR T AA		286	326	367	48	89
CHAI		1	7	J	7	L
PDB		Iqfk	1qfk	lqfk	Iqfk	lqfk
SEQ NO:		1376	1376	1376	1376	1376

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PDB annotation	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSH, COMPLEMENT CONTROL PROTEIN, 2 N-GL YCOSYLATION, MULTI- DOMARN, MEMBRANE ADHESION	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR	SPERMADHESIN ACIDIC SEMINAL PROTBLEN, SPERMADHESIN, BOVINE SEMINAL PLASBA PROTEIN, ACIDIC 2 SEMINAL FLUID PROTEIN, ASPP. CUB DOMAIN, X-RAY CRYSTAL 3 STRUCTURE, GROWTH PACTOR.	COMPLEX (SEMINAL PLASMA PROTEINMENP) SEMINAL PLASMA PROTEINS, SPERMADHEISINS, CUB DOMANN 2 ARCHITECTURE, COMPLEX (SEMINAL PLASMA PROTEINSPP)
Coumpound	HUMAN BETA2- GLYCOPROTEIN I; CHAIN: A;	COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	ASFP; CHAIN: NULL;	MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-1; CHAIN: A; MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-1I; CHAIN: B
SEQFOL D score							
PMF	-0.18	0.35	-0.01	0.94	-0.15	0.48	0.65
Verify score	0.02	0.24	0.29	0.13	0.67	0.64	0.37
Psi Blast	1.7e-46	le-13	3.4e-19	3.4e-11	8.5e-12	3.4e-21	3.4e-22
END AA	444	228	339	445	102	816	222
STAR T AA	41	175	285	407	49	805	608
CHAI	¥.	g	89	щ	æ		В
PDB CI	Iqub	Irfi	irfi	祖	lrfl	1sfp	lspp
SEQ NO ID	1376	1376	1376	1376	1376	1376	1376

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PDR annofation		PLASMINOGEN ACTIVATION	BLOOD COAGULATION FACTOR STUART FACTOR, BLOOD COAGULATION FACTOR, SERNE PROTEINASE, PPIDERMAL 2 GROWTH PACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR, BLOOD COAGULATION FACTOR, SERNE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR, BLOOD COAGULATION FACTOR, SERNE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR, BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH PACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR. STUART FACTOR, BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN	KINASE KINASE, SIGNAL TRANSDUCTION,
Commound	numod mano	T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN; L, C;	CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE; CHAIN: NULL;	CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE;
CEOFOI	D score								61.601
PMR	score	0.04	0.59	0.43	0.69	0.40	0.55	0.71	
Varify	score	0.05	0.09	-0.01	0.25	0.28	0.01	-0.04	
Pei Rlact		1.5e-21	1.76-15	1.76-15	5.1e-20	3.4e-19	3.46-22	5.1e-62	5.1e-62
END	¥	158	230	254	380	444	145	530	534
STAB	TAA	89	131	182	286	367	84	205	236
CHAI	NID		ı	J	1	1	ы		
PUB	A	Itpg	lxka	Ixka	1xka	1xka	lxka	1a06	1a06
OAS	ja ÿ	1376	1376	1376	1376	1376	1376	1381	1381

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PDB annotation	CALCIUM/CALMODULIN	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE	COMPLEX (KINASE/NHIBITOR) CDKE, PIDIKALD; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX KINASE/NHIBITOR)	COMPLEX (INHIBITOR PROTEIN/CRASE) PRHIBITOR PROTEIN, CYCLIA-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHANBETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/WINASI) PHEBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHANBETA, COMBLEX (INHIBITOR PROTEIN/KINASE)	PHOSPHOTRANSFERASE		
Coumpound	CHAIN: NULL;	PROTEIN KINASE CK2/ALPHA- SUBUNIT; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6: CHAIN: A, C, CYCLIN- DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	CYCLIN-DEPENDENT KINASE 6, CHAIN: A; PI9INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CASEIN KINASE-1; 1CSN 4	TRANSFERASE(PHOSPHOTRA NSFERASB) CAMP. DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP 3 (CATALYTIC SUBUNIT) ICTP 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3
SEQFOL D score		84.57		92.79			154.37	
PMF			00.1		00.1	0.74		00:1
Verify score			0.21		0.40	90.0		0.41
Psi Blast		6.8c-40	5.1e-41	1.2e-46	1.2e-46	6.8e-48	3.4e-71	3.4e-71
END AA		550	485	495	485	469	524	498
STAR		161	504	861	199	203	169	196
CHAI N ID		i	<	⋖	v.		Ħ	В
PDB		1860	1bi8	1bix	1blx	lcsn	1ctp	letp
SEQ No:		1381	1381	1381	1381	1381	1381	1381

PDB annotation		PROTEIN KINASE CDK2; TRANSFERASE.	SERINE/THREONINE PROTEIN	KINASE, ATP-BINDING, 2 CELL	PHOSPHORYLATION	PROTEIN KINASE CDK2;	TRANSFERASE, SERINE/THREONINE PROTEIN	KINASE, ATP-BINDING, 2 CELL	CYCLE, CELL DIVISION, MITOSIS,	PHOSPHORYLATION	SERINE/THREONINE-PROTEIN	KINASE CSBP, RK, P38; PROTEIN	SER/THR-KINASE,	SERINE/THREONINE-PROTEIN	SERINE/THREONINE-PROTEIN	KINASE CSBP. RK. P38; PROTEIN	SER/THR-KINASE,	SERINE/THREONINE-PROTEIN	KINASE	TRANSFERASE JNK3;	TRANSFERASE, JNK3 MAP KINASE,	SERINE/THREONINE PROTEIN 2	KINASE	TRANSFERASE JNK3; TD ANSEDD ASE INC. MAD VINASE	SERVICE ENCASE, MAN MAN MAN AND SERVICES,	KINASE	KINASE KINASE, TWITCHIN,	INTRASTERIC REGULATION	KINASE KINASE, TWITCHIN,
Coumpound	(CATALYTIC SUBUNIT) 1CTP 4	HUMAN CYCLIN-DEPENDENT KINASE 2: CHAIN: NULL:				HUMAN CYCLIN-DEPENDENT	KINASE 2; CHAIN: NULL;				P38 MAP KINASE; CHAIN:	NULL;			P38 MAP KINASE: CHAIN:	NULL:				C-JUN N-TERMINAL KINASE;	CHAIN: NULL;			C-JUN N-TERMINAL KINASE;	CILVIE NOLLS		TWITCHIN; CHAIN: A, B;		TWITCHIN; CHAIN: A, B;
SEQFOL D score						115.78					92.87									112,39							127.80		
PMF		1.00													0.88									00.					1.00
Verify		0.39													0.01									0.21					0.52
Psi Blast		1.7e-53				1.7e-53					3.4e-40				3.4e-40					1.7e-46				1.7e-46			1.7e-68		1.7e-68
END		495				499					555				475					577			1	512			570		493
STAR		202				202					183				203					185				203			170		205
CHAI N ID																											٧		Ą
ED GI		Ihcl				Ihci					lian				lian					Ji,				And.			lkob		lkob
SEQ NO ID		1381				1381					1381				1381					1381				1381			1381		1381

PDB annotation	INTRASTERIC REGULATION	TRANSFERASE MITOGEN ACTIVATED REVOTEIN KINASE, MAP 2, ERK2, TRANSFERASE, SERNBETHREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2. ERK2, TRANSFERASE. SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2		COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2	HEAVY CHAIN; CLASS I MHC, T-	CELL RECEPTOR, VIRAL PEPTIDE, 2	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR	COMPLEX (MHC/VIRAL	PEPTIDE/RECEPTOR) HLA-A2	CHIL RECEPTOR VIRAI PEPTIDE 2	COMPLEX (MHC/VIRAL	COMPLEX (MECVIRAL	PEPTIDE/RECEPTOR) HLA A2	HEAVY CHAIN; COMPLEX	(MHC/VIRAL PEPTIDE/RECEPTOR)		COMPLEX (MHC/VIRAL	PEPTIDE/RECEPTOR) HLA A2	(MHC/VIRAL PEPTIDE/RECEPTOR)
Coumpound		EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	EXTRACELLUI.AR REGULATED KINASE 2; CHAIN: NULL;		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN: CHAIN: B:	TAX PEPTIDE; CHAIN: C; T	CELL RECEPTOR ALPHA;	CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	HLA-A 0201; CHAIN: A; BETA-2	MICROGLOBULIN; CHAIN: B;	CELL RECEPTOR ALPHA	CHAIN: D; T CELL RECEPTOR	HLA-A 0201: CHAIN: A: BETA-2	MICROGLOBULIN; CHAIN: B;	TAX PEPTIDE; CHAIN: C; T	CELL RECEPTOR ALPHA;	CHAIN: D; T CELL RECEPTOR BETA: CHAIN: E:	HLA-A 0201; CHAIN: A; BETA-2	MICROGLOBULIN; CHAIN: B;	CELL RECEPTOR ALPHA;
SEQFOL D score			98.67						128.38									143.49		
PMF		0.1			8								1.00							
Verify		0.54			0.39								0.48							
Psi Blast		8.5e-53	8.5e-53		9.6e-54				9.6e-54				3.2e-66					3.2e-66		
END		498	562		210				210				210					210		
STAR T AA		198	213		22				52				52					52		
CHAI N ID		_		1	ы				E				ш					п		
PDB ID		3erk	3erk]	lao7				Tao7				1bd2					1bd2		
SEQ No:		1381	1381	. 000	1384				1384				1384					1384		

PDB annotation		RECEPTOR T CELL RECEPTOR 1BEC 14	RECEPTOR T CELL RECEPTOR IBEC 14	MANUNG SYSTEM HIA-DRI, DRA; HIA-DRI, DRBI 0101; TOR HAII 7 HIA-DRI, DRBI 0101; TOR HAII 7 HIA-DRI, PROTEIN-PROTEIN GOAPLEX, IMMUNOGLOBULIN FOLD	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (RI-AND, HYDROIA-SE 2 MOLECULAR RECOGNITION, BETTOPE MAPPING, LEUCINE-RICH 3 REPROS	COMPLEX (NUCLEAR
Coumpound	CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	HEA CÓCABA HEISTOCOMPATIBILITY ANTIGEN, DR CHAINEA; HLA CLASSI HEISTOCOMPATIBILITY ANTIGEN, DE CHAINE, B; HEBMAGGLUININ HAI BERTIDE CHAN, CHAINE, C; T. CELL, RECEPTOR, ALIPHA CHAINE, CHAINE, D. T. CELL SECEPTOR, ALIPHA CHAINE, CHAINE, D. T. CELL GENERO, BETA CHAINE, CHAINE, E.	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	U2 RNA HAIRPIN IV; CHAIN: Q, COMPLEX (NUCLEAR
SEQFOL D score		130.56				131.76		
PMF			1.00	00'1	1.00		-0.11	-0.01
Verify score			0.49	0.25	0.43		0.04	0.43
Psi Blast		6,4e-66	6.4e-66		9.6e-64	9.6e-64	3.2e-17	3.4e-21
END		210	210	210	210	210	309	156
STAR T AA		52	53	23	50	51	21	26
CHAI N ID				я	В	В	∢	Ą
FDB ID		1bec	Ibec	Tý.	ltcr	Iter	la4y	la9n
SEQ No.		1384	1384	1384	1384	1384	1388	1388

	,									
PDB annotation	PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP, RIBONUCLEOPROTEIN	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL			
Coumpound	R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN; Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A'; CHAIN: A, C; UZ B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	AXONIN-1; CHAIN: A;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;
SEQFOL D score										
PMF		0.19	0.65	0.51	-0.08	90.0	0.89	0.07	0.77	68.0
Verify		0.28	0.48	0.51	0.41	0.42	0.67	-0.15	0.50	0.27
Psi Blast		4.8e-06	1.5e-20	1.3e-05	1.2e-21	4.8e-06	6.8e-20	0.00034	6.4e-27	1.4e-12
END		155	121	106	156	155	121	280	194	128
STAR T AA		46	4	24	56	46	4	11	61	4
CHAI N ID		¥	<	ပ	ပ	o	၁	¥	A	٧
PDB		1a9n	la9n	1a9n	1a9n	la9n	1a9n	lcs6	1d0b	40P1
SEQ NO.		1388	1388	1388	1388	1388	1388	1388	1388	1388

PDB annotation	ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL STRUCTURE, RAB	GERANYLGERANYLTRANSFERASE,	2.0 A 2 RESOLUTION, N.	SUBUNIT, BETA SUBUNIT		TRANSFERASE CRYSTAL STRUCTURE, RAB	GERANYLGERANYLTRANSFERASE,	2.0 A 2 RESOLUTION, N-	FORMYLMETHIONINE, ALPHA	SUBUNIT, BETA SUBUNIT	CONTRACTILE PROTEIN LEUCINE-	RICH REPEAT, BETA-BETA-ALPHA	CHLAMYDOMONAS, FLAGELLA	RNA BINDING PROTEIN TAP (NFX1);	RIBONUCLEOPROTEIN (RNP,RBD	OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	RNA BINDING PROTEIN TAP (NFXI);	RIBONUCLEOPROTEIN (RNP, RBD	OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	RNA BINDING PROTEIN TAP (NFXI);
Coumpound		INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	RAB GERANYLGERANYLTRANSFE	RASE ALPHA SUBUNIT;	CHAIN: A, C; RAB	RASE BETA SUBUNIT; CHAIN:	B, D;	RAB GERANYLGERANYLTRANSFE	RASE ALPHA SUBUNIT;	CHAIN: A, C; RAB	GERANYLGERANYLTRANSFE	RASE BETA SUBUNIT; CHAIN: B, D;	OUTER ARM DYNEIN; CHAIN:	A;		NUCLEAR RNA EXPORT	FACTOR 1; CHAIN: A, B;		NUCLEAR RNA EXPORT	FACTOR I; CHAIN: A, B;		NUCLEAR RNA EXPORT
SEQFOL D score																							
PMF		0.43	0.04	0.90					0.96					-0.02			0.40			0.10			0.04
Verify		0.28	-0.05	0.27					0.59					80.0			-0.05			-0.06			0.26
Psi Blast		1.4e-25	3.2e-25	3.2e-11					1.6e-12					6.4e-13			3.2e-06			4.8e-07			3.2e-06
END		216	236	127					170					236			103			171			103
STAR T AA		63	87	21					46			_		103			41			68			41
CHAI N ID		A	٧	Ą					∢					A			Ą			Y Y			В
PDB		140b	1406	1dce					Idce					6sp1			lfol			1011			lfol
SEQ ID NO:		1388	1388	1388					1388					1388			1388			1388			1388

PDB annotation	RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)			, M. LIGASE CYCLIN A/CDK2- 1, L. ASSOCHATB PROTEIN P45, CYCLIN A/CDK2-ASSOCHATB PROTEIN P19, SKP1, SKP2, F-BOX, LRR, LEUCINE- RCH REPEAT, SCF, DEBQUTIN, 2 E3, UBIOUTIN PROTEIN LIGASE	LIGASE CYCLIN ACDK2- ASSOCIATED P45, CYCLIN ACDK2- ASSOCIATED P49; CYCLIN ACDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBJOUTTN, B3, UBJOUTTN PROFEN LIGASE	LIGÁSE CYCLIN A/CDK2. ASSOCIATED P45, CYCLIN A/CDK2. ASSOCIATED P19; SKP1, SKP2, F. BOX, LRRS, LEUCINE-AUCH REPEARTS, SCF2, DUBOUTTN, B3, UBIOUTTN PROFEN LIGÁSE.	1
Coumpound	FACTOR I; CHAIN: A, B;	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P,	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, I, L, N, P,	SKP2; CHAIN: A, C, E, G, I, K, M, C, SKP1; CHAIN: B, D, F, H, I, L, N, P,	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	
SEQFOL D score							
PMF		80'0-	0.10	-0.15	60.0	0.03	
Verify score		0.29	0.12	0.08	0.21	0.04	
Psi Blast		1.4e-09	1.6e-14	4.8e-11	3.4e-12	1.6e-14	
END		173	213	298	128	213	
STAR		-	8	22	=	50	,
CHAI N ID		<	` V	∢	4	∢	
EDB EDB		lfçv	lfqv	lfqv	1fs2	1fs2	
SEQ NO ID		1388	1388	1388	1388	1388	0000

CHAI	ء جا	STAR T AA	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
								CHAIN: NULL;	RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
	1	47	439	3.2e-20	0.06	-0.15		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
		476	643	1.6e-13	0.05	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
	П	10	22	278.73	95.0	100		TROBONING: CHAIN: NIII I .	MISCI DIBOTIDINI CTAIC, CARDIAC
		2	=	3.26-23	-0.36	10:0		IKOPONIN C; CHAIN: NOLL;	MUSCLE PROTEIN CINC; CARDIAC; MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
		2	19	3.26-22	0.21	0.48		CALMODULIN; CHAIN: NULL;	CALCUM-BINDING PROTEIN CALMODULIN CERUIM TRIC- DOMAIN, RESIDUES 1 - 75; CERUIM- LOADED, CALCUM-BINDING PROTEIN
∢		7	117	4.8e-33	-0.32	0.16		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-BEBENDENT PROTTEN KINA SET IL ICDM A	
		_	132	3.2e-38			53.74	CALCUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
		2	117	3.2e-38	-0.37	0.11		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
<		10	117	1.6e-21	-0.54	0.12		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX- TURN-HELIX
V		2	117	1.6e-35	-0.22	0.23		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER

PDB annotation	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORT PROMATION REGULATION MUSCLE REGULATION MUSCLE CONTRACTION	CALCUMAREGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCUM. BINDING, TROPONIN, E.F. HAND, 2 OPEN CONFORMATION REGULATION AUGUST REGULATION MUSCLE REGULATION MUSCLE CONTRACTION.	CALCIUM-BINDING PROTEIN EF- HAND ITNX 14			CALMODULIN, CALCTUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCTUM-BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCTUM BINDING, HELIX LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCTUM-BINDING PROTEIN/PEPTIDE)	TRANSFERASE RECEPTOR	I TRUSINE KINASE, PROTEIN INTERACTION MODULE, 2
Coumpound	TROPONIN C; CHAIN; NULL;	TROPONIN C; CHAIN; NULL;	TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	EPHA4 RECEPTOR TYROSINE KINASE: CHAIN: A:	KINASE, CHAIN: A;
SEQFOL D score	56.30			51.47		51.68			
PMF		0.11	0.33		0.36		0.27	1.00	
Verify score		-0.35	-0.32		-0.03		-0.42	1.07	
Psi Blast	3.2e-28	3.2e-28	8e-24	4.8c-28	4.8e-28	1,4e-37	1.4e-37	1.7c-24	
END AA	139	Ξ	Ξ	141	111	135	117	1000	
STAR	_	2	2	-	2	_	2	934	
CHAI						∢	٧	٧	
908 01	Incf	Ttof.	Ifnx	1top	ltop	lvrk	lvrk	1b0x	
SEQ El SE	1392	1392	1392	1392	1392	1392	1392	1396	

PDB annotation	DIMERIZATION DOMAIN, TRANSFERASE	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR, HORMONE/GROWTH FACTOR	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE	TRANSFERASE CSK, PROTEIN KINASE, CTERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE	TRANSFERASE CSK, PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN	CYTOKINE G-CSF, G-CSF-R; CLASSI CYTOKINE, HEMATOPOIETIC RECEPTOR, SIGNAL
Coumpound		EPHB2; CHAIN: A, B, C, D, E, F, G, H;	GP130; CHAIN: NULL;	GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B;	TITIN; CHAIN: NULL;	C-TERMINAL SRC KINASE; CHAIN: A;	C-TERMINAL SRC KINASE; CHAIN: A;	C-TERMINAL SRC KINASE; CHAIN: A;	CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A;	GRANULOCYTE COLONY- STIMULATING FACTOR; CHAIN: A, C; G-CSF RECEPTOR;
SEQFOL D score						169.44				
PMF		1.00	0.46	0.01	0.60		1.00	1.00	1.00	0.07
Verify		0.92	0.26	-0.06	0.20		0.83	0.64	0.46	0.40
Psi Blast		8.5e-27	7.5e-22	1.5e-25	4.5e-18	3e-93	1.4e-90	3e-93	66-19	4.5e-35
END		666	537	531	536	668	168	868	531	524
STAR T AA		934	431	328	438	627	628	629	437	328
CHAJ N ID		٧		щ		Y	٧	٧	4	д
PDB		1b4f	16j8	1bp3	1bpv	lbyg	Ibyg	1byg	Ic8p	lcd9
SEQ ID NO:		96EI	1396	1396	1396	1396	9681	1396	96EI	1396

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PDB annotation	TRANSDUCTION	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR	CYTOKINE EBP; ERYTHROPOIETIN RECEPTOR, SIGNAL TRANSDUCTION, CYTOKINE 2 RECEPTOR CLASS 1	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4- HELICAL BUNDLE, ALPHA HELICAL, BUNDLE, TERNARY COMPLEX, EN 2 III DOMAINS, BETA SHEET DOMAINS, CTORKINE-	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-ROTEIN KINASE, ATP- BINDING, 2 PHOSPHORY LATION, RECEPTOR, PHOSPHOTRANSFERASE	PHOSPHOTIANSFERASE FGFRIK, FIBROBIAST GROWTH FACTOR RECEPTOR I; TRANSFERASE, TYROSING-ROTEIN KINASE, ATP- BINDING, 2 PHOSPHORY LATTON, RECEPTOR, PHOSPHOTIANSFERASE	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR I; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP- BINDING 2 BEACKEHOLD VI ATTOM
Coumpound	CHAIN: B, D;	GRANULOCYTE COLONY- STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	ERYTHROPOIETIN RECEPTOR; CHAIN: A, B,	PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	FGF RECEPTOR 1; CHAIN: A, B;	FGF RECEPTOR 1; CHAIN: A, B;	FGF RECEPTOR 1; CHAIN: A, B;
SEQFOL D score					179.56		182.22
PMF		0.63	0.28	0.15		0.1	
Verify		0.32	-0.12	-0.05		0.91	
Psi Blast		6e-19	4.5e-22	4.5e-13	0	0	0
END		531	183	531	006	893	668
STAR T AA		454	338	408	617	621	614
CHAI N ID			∢	O	∢	<	g
10 E		leto	E -	1f6f	ıfçk	Ifgk	Ifgk
SEQ B SO		1396	1396	1396	1396	1396	1396

PDB annotation	RECEPTOR, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE,	TYROSRIE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE,	PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-	ONCOGENE, PHOSPHOTRANSFERASE				CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18	TRANSFERASE P150, C-ABL;	KINASE, KINASE INHIBITOR, STI- 571, ACTIVATION LOOP	COMPLEX	(TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL	TRANSDUCTION,	PHOSPHOTRANSFERASE, 2	SUBSTRATE/ATP ANALOG).	ENZYME, 3 COMPLEX	(TRANSFERASE/SUBSTRATE)	COMPLEX
Coumpound		FGF RECEPTOR 1; CHAIN: A, B;		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;			CELL ADHESION PROTEIN	ADHESION MODULE TYPE III-	10 IFNA 3	FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	PROTO-ONCOGENE	TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	INSUL'IN RECEPTOR; CHAIN: A;	PEPTIDE SUBSTRATE; CHAIN: B;						INSULIN RECEPTOR: CHAIN: A:
SEQFOL D score													188.00							
PMF		1.00		1.00			0.63			-0.05	1.00									00.1
Verify score		0.87		0.88			0.39			80.0	0.71									0.81
Psi Blast		0		0			1.2e-13			3e-26	0		0							0
END AA		\$68		903			524			531	268		016							910
STAR		620		615			454			322	623		623							979
CHAI N ID		В									٧		Ą							Ą
PDB		Ifgk		Ifmk			Ifna			Ifuf	Ifbn		lir3							12
SEQ No:		1396		1396			1396			1396	1396		1396							1396

PDB CHAI STAR END Psi Blast Verify PMF SEQFOL Commpound 1D N ID T AA AA AA score D score D score	STAR END Psi Blast Verify PMF SEQFOL TAA AA score score Dstore	END Psi Blast Verify PMF SEQFOL AA score Score D score	Psi Blast Verify PMF SEQFOL score score D score	Psi Blast Verify PMF SEQFOL score Score D score	PMF SEQFOL score	SEQFOL D score		Coumpoi PEPTIDE SUBSTRA	ınd TE; CHAIN:	PDB annotation (TRANSFERASE/SUBSTRATE)
i ii i	B;	B.	B	B:	B:	B;	B;	B;		TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2
										COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG),
										ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
Imfn 331 533 1.3e-25 0.08 0.53 FIBRONECT	533 1.30-25 0.08 0.53	533 1.30-25 0.08 0.53	1.3e-25 0.08 0.53	0.08 0.53	0.53		FIBRONECT	FIBRONECT	FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD,
										EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING.
										GLYCOPROTEIN
lnuk A 31 202 1.5e-83 0.58 1.00 TYROSIN	31 202 1.5e-83 0.58 1.00	202 1.5e-83 0.58 1.00	1.5e-83 0.58 1.00	0.58 1.00	1.00		TYROSIN	TYROSIN	TYROSINE-PROTEIN KINASE	TRANSFERASE NUK;
RECEPTO	RECEPTO	RECEPTC	RECEPTC	RECEPTC	RECEPTO	RECEPTO	RECEPTO	RECEPTO	RECEPTOR EPH; CHAIN: A;	TRANSFERASE, EPH RECEPTOR TYROSINE KINASE,
lnuk A 31 202 1.5e-83 182.17 TYROSE	31 202 1.5e-83 182.17	202 1.5e-83 182.17	1.5e-83 182.17	182.17	Г	Г	Г	TYROSE	TYROSINE-PROTEIN KINASE	TRANSFERASE NUK;
RECEPT	RECEPT	RECEPT	RECEPT	RECEPT	RECEPT	RECEPT	RECEPT	RECEPT	RECEPTOR EPH; CHAIN: A;	TRANSFERASE, EPH RECEPTOR
										I TRUSINE KINASE,
1qcf A 610 902 0 0.90 1.00 HAEMA	610 902 0 0.90 1.00	902 0 0.90 1.00	0 0.90 1.00	0.90 1.00	1:00		HAEMA	HAEMA	HAEMATOPOETIC CELL	TYROSINE KINASE TYROSINE
VINASE VINASE	MINASE	MINASE	MINASE	MINAGE	MINASE	MINASE	NINASE	MINASE	MINASE (FICE); CFIMIN: A;	DOWN.REGIII ATED KINASE 2
										ORDERED ACTIVATION LOOP
lqg3 A 329 534 1.5e-36 0.19 0.22 INTEGRI	329 534 1.5e-36 0.19 0.22	534 1.5e-36 0.19 0.22	1.5e-36 0.19 0.22	0.19 0.22	0.22		INTEGRI	INTEGRI	INTEGRIN BETA-4 SUBUNIT;	STRUCTURAL PROTEIN INTEGRIN,
CHAIN: A, B;	CHAIN: 7	CHAIN:	CHAIN: 7	CHAIN: 7	CHAIN:	CHAIN:	CHAIN: 7	CHAIN:	, B;	HEMIDESMOSOME, FIBRONECTIN,
										CARCINOMA, STRUCTURAL 2 PROTEIN
19g3 A 331 522 6.8e-11 0.03 0.18 INTEGRI	331 522 6.8e-11 0.03 0.18	522 6.8e-11 0.03 0.18	6.8e-11 0.03 0.18	0.03 0.18	0.18		INTEGRI	INTEGRI	INTEGRIN BETA-4 SUBUNIT:	STRUCTURAL PROTEIN INTEGRIN.
	CHAIN:	CHAIN: A	CHAIN: A	CHAIN: A	CHAIN: A	CHAIN: A	CHAIN: A	CHAIN: A	, B;	HEMIDESMOSOME, FIBRONECTIN,
							-			CARCINOMA, STRUCTURAL 2
										PROTEIN
900 0 0.97 1.00	621 900 0 0.97 1.00	900 0 0.97 1.00	0 0.97 1.00	1.00	1.00		LCK KINA	LCK KINA	LCK KINASE; CHAIN: A;	TRANSFERASE ALPHA BETA FOLD
lqr4 A 331 529 1.5e-30 0.27 -0.03 TENASCII	331 529 1.5e-30 0.27 -0.03	529 1.5e-30 0.27 -0.03	1.5e-30 0.27 -0.03	0.27 -0.03	-0.03		TENASCII	TENASCII	TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIREQUECTIN TYPE, IT HERAPIN
										LIDIOUSE LIIN LIL D-III, MEL PANIS,

Commpound PDB annotation	EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN	PHEIN TYPE RECEPTOR 2. TYCORINE-PROFEST RIVENAE WAR, RECEPTOR OLICOMERICATION, RECHEROR OLICOMERICATION, RECHEROR OLICOMERICATION, RECHEROR OLICOMERICATION, RECHEROR ATTORN, SIGNAL TANKSUCTORN, STRONG, STRONG, PROFESTION, STRONG,	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NAR, 36 STRUCTURES) ITTF 3	VASCULAR ENDOTHELIAL TRANSFERASE KDR; TYROSINE GROWTH PACTOR RECEPTOR KINASE CHAIN: A;	FIBRONECTIN; CHAIN: A, FROTEIN BINDING ED-B, FIBRONECTIN, TYPEII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	FIBRONECTIN; CHAIN: A; FROTEIN BRUDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	HUMAN TISSUE FACTOR; 2HFT COAGULATION FACTOR 4 CHAIN: NULL; 2HFT 5	MATING-TYPE PROTEIN A-1; COMPLEX (TWO DIAA-BINDING CHAIN-ALHA-2; CHAIN-B; COMPLEX (TWO DIAA-BINDING PROTEINS DIAA, COMPLEX (TWO DIAABNING PROTEINS DIAA, COMPLEX, 2 DIAA TRANSCERPTION FRETILA JUDA TRANSCERPTION FRETILA JUDA	
SEQFOL D score		CHAIN	GLYCO (TENT)	YASCULA GROWTH I CHAIN: A;	FIBRO	FIBRO	HUMAN 4 CHAII	MATIN CHAIN PROTEI DNA; C	
PMF Score		1.00	0.25	1.00	-0.14	0.17	-0.18	66.0	
Verify		1.03	0.13	0.88	0.07	0.36	0.22	E	
Psi Blast		1.7e-25	le-17	5.1e-98	3e-09	9e-19	6e-34	90-09	
END		995	524	897	423	529	524	121	
STAR		934	440	. 622	326	439	324	18	
CHAI				٠.	<	<		<	
PDB		lsgg	Ittl	lvr2	2fmb	2fmb	2hft	1akh	
SEQ NO:		1396	1396	1396	1396	1396	1396	1401	

PDB annotation	(DNA-BINDING PROTEIN/DNA), PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	DNA-BINDING PROTEIN ISL-1HD DNA-BINDING PROTEIN, HOMEODOMAIN, LIM DOMAIN	GENE REGULATION PBX1; HOMEODOMAIN	COMFLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION		CORDIFICATION OF THE ACTION OF	DNA-BINDING PROTEIN	
Coumpound		HOMEOBOX PROTEIN HOX-BI; CHAIN: A; PBXI; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	INSULIN GENE ENHANCER PROTEIN ISL-1; CHAIN: NULL;	HOMEOBOX PROTEIN PBX1; CHAIN: A;	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	DNA-BINDING PROTEIN OCT-2 POU HOMEODOMAIN (NMR, AVERAGE STRUCTURE) 1HDP 3	MCM ITANSCRITIONAL REGULATORIC CHARLA, B; MAT ALPHA, 2 TRANSCRITIONAL REPRESSOR, CHARLC, D; STE6 OPERATOR DIM, CHAIN: E, F;	OCT-3; IOCP 5 CHAIN: NULL; 10CP 6	DNA BINDING PROTEIN OCT-I POU HOMEODOMAIN DNA- BINDING PROTEIN MITTANT
SEQFOL D score									
PMF		0.43	0.93	0.03	66.0	0.80	0.00	0.84	96:0
Verify		0.27	0.73	-0.11	0.82	0.50	0.63	0.28	0.41
Psi Blast		0.0006	6e-05	0.0003	0.0003	0.00015	0.00015	96-96	0.0001
END		125	125	127	125	125	125	125	125
STAR T AA		æ	83	88	88	8	52	83	83
CHAI		æ		<	m		.'		
E G		1672	1bw5	1du6	<u></u>	lhđp	m m	10cp	lpog
SEQ No ib		1401	1401	1401	1401	1401	1401	1401	1401

PDB annotation		COMPLEX (ISOMERASE/DNA) COMPLEX (ISOMERASE/DNA), DNA, TOPOISOMERASE I	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	LIPID BINDING PROTEIN APOE3; LIPID TRANSPORT, HEPARIN- BINDING, PLASMA PROTEIN, HDL, VLDL	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	SERUM PROTEIN ACRP30 CIQ TNF TRIMER ALL-BETA, SERUM PROTEIN	SERUM PROTEIN ACRP30 CIQ TNF TRIMER ALL-BETA, SERUM PROTEIN	SERUM PROTEIN ACRP30 CIQ TNF TRIMER ALL-BETA, SERUM PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22
Coumpound	WITH IPOG 3 ARG GLY SER HIS MET INBERFED AT THE IN- TERMINUS AND ASP ILE IPOG 4 INSERTED AT THE C. TERMINUS (INSRASHAL RG)LNS(16-D1) IPOG 5 (IMR, RG)LNS(16-D1) IPOG 5 (IMR,	TOPOISOMERASE I; CHAIN: A; DNA; CHAIN: B, C;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	APOLIPOPROTEIN E; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A. B. C.	30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score									
PMF		-0.09	0.00	0.19	0.04	0.39	-0.13	0.43	0.29
Verify		0.03	-0.16	-0.13	-0.12	1.14	0.71	0.84	-0.03
Psi Blast		5.1e-08	0.00017	0.00017	6e-15	le-27	6e-22	4.5e-18	66-12
END		772	556	634	551	947	947	947	591
STAR T AA		644	389	222	367	826	827	826	375
CHAI		4	æ	¥.	4	A	В	2	A
PDB CI		1a36	1dn1	lor3	ldm	1c28	1c28	1c28	lcun
SEQ Signal		1403	1403	1403	1403	1404	1404	1404	1404

			_	,			
PDB annotation	TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA FIELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRICTIRA, I PROTEIN	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	GROWTH FACTOR NEU DIFFERENTIATION FACTOR (RAT), ACETYLCHOLINE GROWTH FACTOR		COMPLEX (ISOMERASE/PROTEIN KINASI) FREPI; SERNETHECONINE-PROTEIN KINASE REGETOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECCHEN 2 SERINETHREONINE KINASE	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
Coumpound		ALPHA SPECTRIN; CHÁIN: A, B, C;	SSO1 PROTEIN; CHAIN: A;	HEREGULIN-ALPHA; CHAIN: NULL;	GROWTH FACTOR HEREGULIN-ALPHA (EPIDERMAL GROWTH FACTOR-LIKE DOMAIN) IHRE 3 (NMR, MINIMIZED A VERAGE STRUCTURE) IHRE 4	FK306-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	FGF RECEPTOR I; CHAIN: A, B;
SEQFOL D score							
PMF		0.03	61.0	0.11	0.25	0.12	0.04
Verify score		0.02	-0.08	0.07	0.13	-0.26	-0.02
Psi Blast		4.5e-07	6e-07	0.0045	0.0045	1.4e-09	1.7e-05
END		651	467	150	150	129	126
STAR		436	292	120	120	25	22
CHAI N ID		∢	A			Ф	¥
PDB		Icun	1flo	lhae	1hre	1b6c	Ifgk
SEQ GI ÖN		1404	1404	1404	1404	1407	1407

			T			<u>a</u>	Г				Т
PDB annotation	PHOSPHOTZANSTERASE C-SRC, PHOSPHOTZANSTERASE C-SRC, PROSP OR WT. ATTON, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSTERASE PHOSPHOTRANSTERASE	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI- 571, ACTIVATION LOOP	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP	TRANSFERASE ALPHA BETA FOLD	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2, TRANSFERASE, SERNPETHREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2		LIPID-BINDING PROTEIN PEBP, PBP LIPID-BINDING	LIPID-BINDING PROTEIN PEBP, PBP LIPID-BINDING	LIPID-BINDING LIPID-BINDING, SIGNALLING	LIPID-BINDING LIPID-BINDING,
Соимрони	TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	ERK2; CHAIN: NULL;	HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	LCK KINASE; CHAIN: A;	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;		PHOSPHATIDYLETHANOLAMI NE-BINDING PROTEIN; CHAIN: NULL;	PHOSPHATIDYLETHANOLAMI NE-BINDING PROTEIN; CHAIN: NULL;	PHOSPHATIDYLETHANOLAMI NE BINDING PROTEIN; CHAIN: A, B:	PHOSPHATIDYLETHANOLAMI
SEQFOL D score									267.15		271.38
PMF	0.36	0.18	0.37	0.11	0,23	0.09		1.00		1.00	
Verify	0.17	-0.09	-0.12	-0.56	-0.75	-0.35		09:0		0.89	
Psi Blast	3e-05	1.58-05	7.5e-06	9e-05	7.5e-05	1.5e-05		4.5e-70	4.5e-70	3e-68	3e-68
END	127	130	131	129	61	126		168	168	168	891
STAR T AA	22	22	21	22	22	21		2	2		3
CHAI N ID		¥		∢	٧					<	<
PDB ID	Ifmk	ndJI	Ipme	1qcf	lqpc	3erk		1844	1844	1beh	lbeh
SEQ No id	1407	1407	1407	1407	1407	1407		1408	1408	1408	1408

PDB annotation		HALOPEROXIDASE BROWOPEROXIDASE L, HALOPEROXIDASE L; HALOPEROXIDASE, OVINOBENIZA 6E	HALOPEROXIDASE HALOPEROXIDASE; HALOPEROXIDASE; OXIDOREDUCTASE; PROPIONATE COMPLEX	AMINOPEPTIDASE AMINOPEPTIDASE, PROLINE IMINOPEPTIDASE, SERINE PROTEASE, 2 XANTHOMONAS CAMPESTRIS	AMINOPEPTIDASE AMINOPEPTIDASE, PROLINE IMINOPEPTIDASE, SERINE PROTEASE, 2 XANTHOMONAS CAMPESTRIS	HYDROLASE HYDROLASE, HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE	HYDROLASE HYDROLASE, HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE	HYDROLASE AB HYDROLASE FOLD, DEHALOGENASE I-S BOND	HYDROLASE LINB, 1,3,4,6- TETRACHLORO-1,4- CYCLOHEXADIENE
Coumpound	A,B;	CHLOROPEROXIDASE L; CHAIN: A, B, C;	CHLOROPEROXIDASE F; CHAIN: NULL;	PROLINE IMINOPEPTIDASE; CHAIN: A, B;	PROLINE IMINOPEPTIDASE; CHAIN: A, B;	HALOALKÁNE DEHALOGENASE; CHAIN: NULL;	HALOALKANE DEHALOGENASE; CHAIN: NULL;	HALOALKANE DEHALOGENASE; 1. CHLOROHEXANE CHAIN: A;	HALOALKANE DEHALOGENASE; CHAIN: A;
SEQFOL D score				60.20		61.14			
PMF		0.90	0.45		0.42		0.77	0.99	0.19
Verify score		0.25	0.13		0.00		0.13	0.38	-0.16
Psi Blast		0.00015	9e-08	4.5e-05	4.5e-05	1.5e-08	1.5e-08	60-09	3e-05
END		319	319	319	319	325	318	319	154
STAR T AA		47	47	11	47	12	35	10	47
CHAI		∢		V V	V V			<	V
PDB ID		1a88	la8s	lazw	Iazw	1b6g	1b6g	loqw	lcv2
SEQ NO.		1410	1410	1410	1410	1410	1410	1410	1410

DISUBSTITUTED UREA 2 INHIBITOR DISUBSTITUTED UREA 2 INHIBITOR PSEUDOMONADACEAE, COVALENT ANALOGUE, ENANTIOSELECTIVITY CYANHYDRIN FORMATION, LYASE BIODEGRADATION, ALPHA/BETA-ALPHA/BETA HYDROLASE FOLD, OXYNITRILASE, CYANOGENESIS, INTERMEDIATE, 2 TRIGLYCERIDE ALPHA/BETA HYDROLASE FOLD, CONFORMATION, 2 HYDROLASE, HYDROLASE FOLD, PROLINE, PROLYL AMINOPEPTIDASE, 2 HYDROLASE FOLD, PROLINE, PROLYL AMINOPEPTIDASE, 2 SERRATIA, IMINOPEPTIDASE LIPASE LIPASE; LIPASE, SERRATIA, IMINOPEPTIDASE PSEUDOMONADACEAE, CIS-LYASE OXYNITRILE LYASE; ENDOCYTOSIS/EXOCYTOSIS DEHALOGENASE, LINDANE, HYDROLASE HOMODIMER. HYDROLASE ALPHA BETA HYDROLASE HOMODIMER, HYDROLASE ALPHA BETA NSECI; PROTEIN-PROTEIN PDB annotation HYDROLASE LIPASE PEPTIDE, CLOSED HYDROLASE, TYDROLASE HYDROLASE 9 EPOXIDE HYDROLASE: CHAIN: LIPASE, GASTRIC; CHAIN: A, B; EPOXIDE HYDROLASE; CHAIN: SYNTAXIN BINDING PROTEIN PROLYL AMINOPEPTIDASE; PROLYL AMINOPEPTIDASE; I; CHAIN; A; SYNTAXIN 1A; IYDROXYNITRILE LYASE; TRIACYL-GLYCEROL-HYDROLASE; CHAIN: D, E; HYDROLASE; CHAIN: D; చ HYDROLASE; CHAIN: Coumpound RIACYLGLYCEROL IRIACYL,GL,YCEROI CHAIN: A; CHAIN: A; CHAIN: A; À, B; A, B; SEQFOL D score 57.92 PMF score 0.98 95 0.37 0.12 0.05 Verify score -0.02 90.0 0.12 0.14 0.02 Psi Blast .2e-05 0.00045 1.2e-05 .1e-07 0.0006 3e-07 9e-09 **3e-05** 0.003 END ¥ 8 8 316 155 513 STAR T AA 384 4 47 4 4 4 7 47 CHAI A E œ ala ⋖ ⋖ Д മ K PDB leki lhlg ldnI a E. lqge lqj4 4lip 븀 븅 410 1410 1410 1410 1410 1410 1415 ΑŞ 1410

SEQ NO.	EDB EDB	CHAI	STAR T AA		END Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
									CHAIN: B;	COMPLEX, MULTI-SUBUNIT
1418	lath	<	401	426	0.00015	0.11	0.01		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1418	lalh	∢	404	485	3e-24	0.05	0.95		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1418	Imey	υ	403	486	4.56-25			76.20	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	Ітеу	ပ	404	485	4.5e-25	-0.09	00:1		DNA; CHAIN: A, B, D, B; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	Imey	υ	432	543	60-23	-0.01	0.53		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	Imey	υ	461	575	1.2e-21	-0.31	90.0		DNA; CHAIN: A, B, D, B; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	lgpl		222	547	1.2e-06	-0.44	0.25		SPIF3; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1418	Inbd	ပ	408	543	1.4e-24	-0.01	0.07		YYI; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION

						د ا	
PDB annotation	REGULATION/DNA) YING-YANG I; TRANSCRETPON METITATION, INITATOR ELEMENT, YY, ZINCZ FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIFTION)	COMPLEX (TRANSCRIPTION IN TRANSCRIPTION IN TRANSCRIPTION INTIATION, INTIATION, INTIATION, INTIATION, INTIATION, INTIATION ELEMENT, YYI, ZINC2 FINGER REOTEIN, DAN-EX (TRANSCRIPTION, 3 COMPLEX (TRANSCRIPTION)	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR		COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI ZINC FINGER COMPLEX (DNA-
Coumpound	ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CRAIN; C; ADBNO- SASOCIATBO VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	ADRI; CHAIN: NULL;	ADRI; CHAIN: NULL;	COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D score							
PMF		0.03	0.17	0.03	0.06	0.47	0.25
Verify score		-0.42	0.04	-0.41	-0.69	-0.05	-0.16
Psi Blast		1e-24	4.5e-14	1.4e-12	1.2e-14	3e-20	4.5e-33
END		575	549	575	27.7	485	575
STAR T AA		432	461	225	222	369	404
CHAI		o			¥	∢ .	<
EDB CD		1ubd	2adr	2adr	2drp	2gli	2gli
SEQ NO:		1418	1418	1418	1418	1418	1418

PDB annotation BINDING PROTEINDINA) COMULEX RELOOD HYDROLAES, SEGNE TOPROCIACE STANDEN A TOPROCIACE STANDEN COMPLEX RELOOD ANTITIONEN RELOOD ANTITIONEN RELOOD COMULETIONEN RELOOD ANTITIONEN RELOOD RELOOD RELOOD ANTITIONEN RELOOD COMULETIONEN RELOOD COMULETIONEN RELOOD RELOOD RELOOD ANTITIONEN RELOOD COMULETIONEN RELOOD	
PAMAI; PAMAI; PAMAI; PAMAIN	SIS FACTOR
Coumpound Caupound ACTIVATED PROTEIN C; CHAIRE F, CHAIRE F, CHAIRE T, D. PHEPTRO-MAI, EACTOR VILL, CHAIRE THE LANG FLACTOR VILL, CHAIRE THE LANG CHAIRE TO DEPTREAMEN FLACTOR VILL, CHAIRE THE LANG CHAIRE TO DEPTREAMEN CHAIRE AS TO DETRETTE AND CHAIRE AND LOST CHAIRE CHAIRE AS L. D. FIREOMEN CHAIRE AS L. L. THROMEN CHAIRE AS L. L. L. L. THROMEN CHAIRE AS L. L. L. L. THROMEN CHAIRE AS L.	TUMOR NECROSIS FACTOR
SEQPOL. D score 57.15	
0.25 0.55	-0.11
Score 0.04	0.14
Pal Blast 30-15 15-15 10-17	3e-16
AA AA 239 232 232 264	161
174A 118 136 136	31
N N D L L L L L L L L L L L L L L L L L	٧
D Iden Iden Ides	lext
NO. 1419 1419 1419	1419

PDB annotation	PROTEIN	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	COAPILEY (BLOOM) CHRISTMAR FACTOR; COMPILEX, INTERITOR, HEMBETOR; COMPILEX, INTERITOR, HEMBETOR, HEMBETOR, HEMBETOR, HEMBETOR, HEMBETOR, HEMBETOR, AS HEASING, SERUNE PROTEASE, CALCIUM, BINDING, HYDROLASE, 3 GLYCOPROTEN	COAPT EX (BLODD) COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPILEX, INHIBITOR, HENDEPHILLAGER, BLODD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIM- BRODING, HYDROLASE, 3	COMPLEX (BLOD) COAGULATION/INHIBITOR) CHRISTMAR FACTOR; COMPLEX, INHIBITOR; HEMPORTILA/EGF, BLODD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCUM- BINDING, HYDROLASE, 3 GLYCOPROPENT	COMPLEX (BLOOD
Coumpound		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	FACTOR IXA; CHAIN: C, L,; D- PHE-PRO-ARG; CHAIN: I;	FACTOR IXA; CHAIN: C. L.; D. PHE-PRO-ARG; CHAIN: I;	FACTOR IXA; CHAIN: I; PHE-PRO-ARG; CHAIN: I;	FACTOR IXA; CHAIN: C, L,; D-
SEQFOL D score		59.06				78.19			67.49	
PMF			-0.01	-0.01	0.23		-0.09	0.18		0.31
Verify			0.05	0.54	0.51		0.07	-0.04		-0.30
Psi Blast		3e-16	9e-22	4.5e-26	4.5e-27	4.5e-27	1.16-25	6e-21	6e-30	6e-30
END		243	298	185	247	234	128	298	165	223
STAR T AA		19	125	59	19	- 44	13	205	38	2/2
CHAI N ID		Ą					L	ı	ī	1
an G		1ext	1klo	1klo	1klo	Iklo	1pfx	lpfx	1pfx	1pfx
SEQ NO:		1419	1419	1419	1419	1419	1419	1419	1419	1419

PDB CHAI STAR END PSI ID NID TAA AA	STAR END T AA AA	END			Psi Blast	Verify	PMF score	SEQFOL D score	Coumpound	PDB annotation
										CHRINARS FACTORIS, COMPLEX, INTIBETOR, HEMOPHILIAEGE, BLOOD COAGULATION, 2 PLASMA, SERINE PROTFASE, CALCUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
1pp2 R 39 169 1.5c-19 0.24	39 169 1.5e-19	169 1.5e-19	1,5e-19		0.24		-0.18		HYDROLASE CALCIUM-FREE PHOSPHOLIPASE A=2= (E.C.3.1.1.4) 1PP2 4	
iqk L 109 216 3e-15 0.11	109 216 30-15	216 3e-15	36-15		0.11		0.30		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPETIDYL INHIBITOR; CHAIN: C;	SERDIE PROTEASE FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1qR L 145 247 7.5c-15 0.09	145 247 7.50-15	247 7.56-15	7.56-15		60:00		-0.06		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL, INHIBITOR; CHAIN: C;	SERNE PROTEASE FVIIA; BLOOD COAGULATION, SERINE PROTEASE
iskz 141 271 3e-15 -0.17	271 36-15	271 36-15	3e-15		-0.17		86'0		ANTISTASIN; CHAIN: NULL;	SERNINE POOTTAGES IN HIBITOR FACTOR XA INHIBITOR; ANTISTAGIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
18kz 66 179 30-15	621	621		36-15				55.31	ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, ORYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
ttpg 156 237 4.5e-20 0.31	237 4.5e-20	237 4.5e-20	4.5e-20	П	0.31	П	0.53		T-PLASMINOGEN ACTIVATOR	PLASMINOGEN ACTIVATION

									T	
PDB annotation		PLASMINOGEN ACTIVATION	PLASMINOGEN ACTIVATION	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE	NEUROTOXIN PHOSPHOLIPASE A2 INHIBITOR, X-RAY STRUCTURE, RECOGNITION, 2 MOLECULAR EVOLUTION, NEUROTOXIN	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN		OXIDOREDUCTASE CPR, P450R; X-RAY CRYSTALLOGRAPHY, FLAVOPROTEIN, NITRIC OXIDE SYNTHASE, 2 OXIDOREDUCTASE	OXIDOREDUCTASE TWO DOMAIN MOTTE, ROSSMANN FOLD
Coumpound	F1-G; ITPG 7 CHAIN: NULL; ITPG 8	T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PHOSPHOLIPASE A2; CHAIN: A, B;	PHOSPHOLIPASE A2; CHAIN: A, B;	PHOSPHOLIPASE A2 INHIBITOR; CHAIN: NULL	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	NADPH-CYTOCHROME P450 REDUCTASE; CHAIN: A, B;	CHLOROPLAST FERREDOXIN- NADP+ OXIDOREDUCTASE; CHAIN: A, B;
SEQFOL D score										
PMF		0.18	-0.01	-0.19	-0.19	-0.18	0.37	0.30	0.01	0.21
Verify		-0.31	0.14	0.02	0.04	0.07	0.17	0.23	-0.16	-0.13
Psi Blast		4.5e-15	7.5e-19	9e-16	7.5e-16	3e-19	9e-14	1.5e-24	6.8e-40	5.1e-57
END AA		297	109	273	236	204	222	142	539	538
STAR T AA		220	29	145	81	81	145	13	272	252
CHAI N ID				A	A		1	A	V V	Ą
PDB		ltpg	ltpg	lvap	lvap	lvpi	lxka	9wga	lamo	1603
SEQ ID NO:		1419	1419	1419	1419	1419	1419	1419	1421	1421

PDB annotation	(%)) St., 372	IAIN: OXIDOREDUCTASE RIBOFLAVIN, FLAVIN REDUCTASE SUPERFAMILY, OXIDOREDUCTASE	B; FLAVOENTYME, PHOTON THAVOENTYME, PHOTOSYNTHESIS, ELECTRON TRANSFER, HYDRIDD 2 TRANSFER, OXIDOREDUCTASE	ILI; OXIDOREDUCTASE FINR; OXIDOREDUCTASE, FAD, FLAVOPROTEIN, NADP, FAD, THYLAKOID MEMBRANE, 2 HYCOBLISOME, FINR, NADP+ REDUCTASE	OR) WITE OMB 3	TDE; COMPLEX (ZINC FINGER/DNA)
Coumpound	OXIDOREDUCTASE (MADPHA,IERREDOXIN(A)) FERREDOXIN-MADP+ OXIDOREDUCTASE (FERREDOXIN REDUCTASE, IFNB 3 FLAVORNZYME) (E.C.11.81.2) IFNB 4 IFNB 7.	FLAVIN REDUCTASE; CHAIN: A, B, C, D;	FERREDOXIN:NADP+ REDUCTASE; CHAIN: A, B;	FERREDOXINNADP+ REDUCTASE; CHAIN: NULL;	OXIDORED/CTASE (NITROGENOUS ACCEPTOR) NADH-DEPENDENT WITRATE REDUCTASE (CYTOCHROME B REDUCTASE (CYTOCHROME B) REAGMENT) (E.C.1.6.6.1) COMPLEXED WITH FAD 2CND 4 (SYNCHROTRON X-RAY DIFFRACTION) 2CND 5	QGSR ZINC FINGER PEPTIDE;
SEQFOL D score						80.07
PMF	0.01	0.07	0.43	-0.03	-0.12	
Verify score	0.09	-0.07	-0.14	0.06	0.00	
Psi Blast	3.4e-55	3.4e-31	1.7e-54	3.4e-49	3.4e-57	1.5e-45
END	538	510	537	538	502	347
STAR T AA	252	246	252	258	244	265
CHAI N ID		۷.	¥			4
EDB EDB	1fib	lqf)	1qfz	1que	2cnd	lalh
SEQ EQ EQ	1421	1421	1421	1421	1421	1426

PDB annotation	NG ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PRCTEN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	CANGE THOREADTH ON COMPLEX (TRANSCRIPTION REGULATIONNAL) COMPLEX (TRANSCRIPTION REGULATIONNAL) ROAD POLYMERASE III, 2 ITANSCRIPTION INTIATION, ZINC FINANCE PROPER III, 2 ITANSCRIPTION INTIATION, ZINC FINANCE PROPER III, 2			COMPLEX (TRANSCRIPTION BE; FACTORIVAL TRANSCRETTION FACTOR, PROTEIN-DNA COMPLEX, CYTORINE 2 ACTIVATION COMPLEX (TRANSCRIPTION FACTORIONA)	(**************************************
Coumpound	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TFIIA; CHAN; A, D; SS RIBOSOMAL RNA GENE; CHAIN; B, C, E, F;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DINA; CHAIN: A, B;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;	
SEQFOL D score		103.77	99.56	88.81	93.51		
PMF						0.27	01.0
Verify score						0.41	200
Psi Blast		le-51	1.7e-38	66-54	69-99	0.00034	10.00
RND		318	402	318	347	320	200
STAR T AA		236	236	211	207 .	191	107
CHAI		ပ	<	O	V	A	~
PDB		Imey	1476	lubd	2gli	1bg1	1 brd
SEQ NO.		1426	1426	1426	1426	1434	1434

	STAR T AA	END	Psi Blast	Verify	PMF score	SEQFOL D score	Coumpound	PDB annotation
								LIPID IKANSPORT, LIPID TRANSPORT, HEPARIN-BINDING, PLASMA 2 PROTEIN, HDL, VLDL REMARK
		514	1.5e-27			115.08	COLICIN IA; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
127		372	7.5e-11	0.07	-0.01		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
228		430	3e-10	0.28	0.00		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HIELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COLLED-COLLS, STRUCTURAL PROTEIN
253		475	3e-11	0.10	0.10		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
389		494	6e-06	0.40	0.40		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COLLED-COILS, STRUCTURAL PROTEIN
296		481	6e-11	0.05	0.18		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
316		449	1.5e-08	0.18	-0.18		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX

SEQ ID NO:	EDB TD	CHAI	STAR T AA	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
										BUNDLE
1434	lez3	<	364	486	1.50-08	0.36	-0.02		SYNTAXIN-IA; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1434	lqsa	¥	2	514	3e-20			104.88	SOLUBLE LYTIC TRANSGLYCOSYLASE SLT70; CHAIN: A;	TRANSFERASE ALPHA- SUPERHELIX, TRANSFERASE
1434	lquu	¥	228	464	1.5e-18	0.21	0.27		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN
1434	lquu	4	332	481	1.2e-09	0.25	-0.17		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN
1434	lsig		225	512	3e-09			88.68	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMATO; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1434	Isig		293	514	3e-09	0.14	0.21		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70, RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1437	lrgp		1126	1315	1.5e-53			105.03	RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE- ACTIVATING PROTEIN, G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
1437	ltx4	⋖	1129	1329	4.5e-58			106.55	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATIVE ROTO-CONCOGENE) GTPASE-ACTIVATING PROTEIN RHGGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GPASE, 2 TRANSITION STATE, GAP
Ī										
1441	lann		7	299	0			431.20	ANNEXIN IV; 1ANN 5 CHAIN:	CALCIUM/PHOSPHOLIPID-BINDING

PDB CHAI STAR END ID NID TAA AA	STAR END TAA AA	END			Psi Blast	Verify	PMF score	SEQFOL D score	Coumpound	PDB annotation
·		·							NULL; IANN 6	PROTEIN 2.3 S TO CALELECTRIN, ENDONEXIN; I ANN 7 32.5KD CALELECTRIN, ENDONEXIN; I, LIPOCORTIN IV, IANN 12.2 CHROMOBINDIN IV, PROTEIN II IANN 13
1dhr 9 213 6.8e-55	213	213		6.8e-55				304.31	OXIDOREDUCTASE(ACTING ON NADH OR NADPH)	
									DIHYDROPTERIDINE	
									(E.C.1.6.99.10) COMPLEX IDHR 3 WITH NADH IDHR 4	
						_				and the state of t
1b7f A 1 151 3.4e-33 0.38	1 151 3.4e-33	3.4e-33	3.4e-33		0.38	1	0.54		SXL-LETHAL PROTEIN; CHAIN: A. B: RNA (5'-	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA: SPLICING
									R(P*GP*UP*UP*GP*UP*UP*UP*	REGULATION, RNP DOMAIN, RNA
1b7f A 73 230 6.8e-21 0.38	73 230 6.8e-21	230 6.86-21	6.8e-21	Ť	0.38	Γ	000		SXI-I ETHAI PROTEIN: CHAIN:	RNA-RINDING PROTEIN/RNA TRA
			i				3		A, B; RNA (5'-	PRE-MRNA; SPLICING
									R(P*GP*UP*UP*GP*UP*UP*UP* UP*UP*UP*UP*UP*U)-CHAIN: P. O:	REGULATION, RNP DOMAIN, RNA COMPLEX
1b7f A 73 252 6.8e-21	73 252	252	-	6.8e-21		Γ		51.11	SXL-LETHAL PROTEIN; CHAIN:	RNA-BINDING PROTEIN/RNA TRA
									A, B; RNA (5'-	PRE-MRNA; SPLICING
									K(P*GP*UP*UP*GP*UP*UP*UP* UP*UP*UP*UP*UP*U)- CHAIN: P, Q;	KEGULATION, KNP DOMAIN, KNA COMPLEX
lcvj A I 156 3.4e-46	1 156	-	-	3.4e-46		Γ		52.06	POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A)
				_					PROTEIN 1; CHAIN: A, B, C, D,	BINDING PROTEIN 1, PABP 1; RRM,
			******						E, F, G, H; RNA (5'-	PROTEIN-RNA COMPLEX, GENE
									K(*AP*AP*AP*AP*AP*AP*	KEGULATION/KNA
									AP*AP*AP*A)-5']; CHAIN: M, N, O, P, Q, R, S, T;	
levj A 5 157 3.4e-46 0.27	5 157 3.4e-46	157 3.4e-46	3.4e-46		0.27		08.0		POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A)
						٦			PROTEIN 1; CHAIN: A, B, C, D,	BINDING PROTEIN 1, PABP 1; RRM,

PDB annotation	PROTEIN-RNA COMPLEX, GENE AP* REGULATION/RNA M, N,	GENE REGULATION/RNA POLY(A) DE BINDING PROTEIN I. PASP 1; RRM, PROTEIN-RNA COMPLEX, GENE AP* REGULATION/RNA M. N,	i GENE REGULATION/RNA POLY(A) , D, BINDING PROTEIN , PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE AP* REGULATION/RNA	GENE REGULATION/RNA POLY(A) , D. BINDING PROTEIN , PASP 1, RRM, PROTEIN-RNA COMPLEX, GENE AP* REGULATION/RNA	GENE REGULATION/RNA POLY(A) D, BINDING PROTEIN 1, PASP 1, RRM, PROTEIN-RNA COMPLEX, GENE AP* REGULATION/RNA	GENE REGULATION/RNA POLY(A) , D, BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE AP* REGULATION/RNA AN, A, N,
Coumpound	E. F. G. H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, B, F, G, H, RN4 (5* R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, B, F, G, H, RNA (5* R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H, RNA (5* R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*J; CHAIN: M, N, AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, B, F, G, H, RNA (5* R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP; S); CHAIN: M, N, AP*AP*AP*AP; 1;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5*- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A
SEQFOL D score				,		
PMF score		0.31	0.59	0.15	00.1	0.19
Verify score		0.02	0.25	0.08	0.74	-0.03
Psi Blast		5.1e-24	6.8e-40	1.7e-21	1.7e-19	1.7e-31
END		256	137	230	159	130
STAR		77	w	4	11	s
CHAI N ID		¥	ф	Д	Ľ.	Ħ
FDB CI		levj	lovj	levj	levj	levj
S e S		1452	1452	1452	1452	1452

PDB annotation	GENE REGULATIONRNA POLY(A) BNDING PROTEIN I, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATIONRNA	RNA BINDING PROTEIN RNA- BINDING DOMAIN	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RN BINDING, 2 RIBONUCLEOPROTEIN	NUCLEAR PROTEIN HEITROGENBOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNB ANDING, 2 RIBONUCLEOPROTEIN	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN	COMPLEX (RIBONUCLEOPROTEIN/DNA) (RIBONUCLEOPROTEIN/DNA), I BETREOGREDOUS NUCLEAR 2 RIBONUCLEOPROTEIN AI	RNA BINDING DOMAIN RNA BRDDNG DOMARI, RBB, RNA RECOGNITION MOTIF, RKM, 2 SPLICING INHIBITOR, SEX 3 TRANSLATIONAL INHIBITOR, SEX 3
Coumpound	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, R, C, G, H; RNA (5** R(*AP*AP*AP*AP*AP*AP*AP*AP* P*AP*AP*AP*AP*AP* O, P, Q, R, S, T;	HU ANTIGEN C; CHAIN: A;	HNRNP A1; CHAIN: NULL;	HNRNP A1; CHAIN: NULL;	SPLICING FACTOR UZAF 65 KD SUBUNIT; CHAIN: A;	HETEROGENEOUS NITCLEAR RIBONUCLEOPROTEIN AI; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	SEX-LETHAL; CHAIN: A, B, C;
SEQFOL D score					50.59		
PMF	1.00	1.00	0.07	00.1		0.64	0.04
Verify	0.81	0.73	0.06	0.87		0.28	0.13
Psi Blast	1.7e-19	1.7e-21	1.7e-35	1.7e-21	3.4e-19	1.2e-36	3.4e-32
END	159	153	151	157	158	155	144
STAR T AA	t.	7.3	-	75	74	-	
CHAI N ID	H	∢			V	∀	¥
EDB CO	lcvj	Z8PI	IhaI	lha1	2u2f	2up1	3sxl
Se o	1452	1452	1452	1452	1452	1452	1452

				_				_
PDB annotation	DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHBITOR, TRANSLATIONAL INHBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSIA/TIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION		TRANSFERASE HIV-1 REVERSE TRANSCRIPTASB, AIDS, NON- NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON- NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN	TRANSFERASE HIV-I REVERSE TRANSCRIPTASE, AIDS, NON- NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN	TRANSFERASE/IMMUNE SYSTEM/DNA HIV-1 RT; HIV-1 RT;
Coumpound		SEX-LETHAL; CHAIN: A, B, C;	SEX-LETHAL; CHAIN: A, B, C;	!	HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B:	HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	HIV-1 REVERSE TRANSCRIPTASE (CHAIN A);
SEQFOL D score			53.30					
PMF score		69'0			0.87	0.84	66.0	0.99
Verify score		0.20			-0.04	-0.17	-0.09	-0.06
Psi Blast		1.4e-20	3.4e-32		3.46-85	5.1e-88	0	1.7e-91
END		230	146		899	899	899	671
STAR T AA		96	7		345	346	345	341
CHAI N ID		∢	∢		∢	æ	æ	A
PDB		3sxl	3sxl		1c0t	1001	1010	1c9r
SEQ No io		1452	1452		1454	1454	1454	1454

Coumpound PDB annotation	CHAIN: A, HIV-1 REVERSE HIV, REVERSE TRANSCRIPTASE, CHANNE, METISHELE, AC, ROOTEN-DNA 2, CHANNE, ANTIBODY (LIGHT COMPILEZ, DRUG RESSTRANCE, ANTIBODY (LIGHT COMPILEZ, DRUG RESSTRANCE, HIRAY CHANN; CH	TRANSPERABLOANDANINE TRANSPERA	BERURSET TRANSCRIPTASE HIV. IREVREGE TRANSCRIPTASE (AMINO- TREMINAL JUE (FINIGRES HIARS AND PALA HIARS AND PALA	MMLV REVERSE REVERSE TRANSCRIPTASE TRANSCRIPTASE; 1MML 4 CHAIN; NULL; 1MML 5	MMLV REVERSE REVERSE TRANSCRIPTASE	TRANSCRIPTASE; 1MML 4 CHAIN: NULE; 1MML 5	RANSCRIPASE; IMML4 CHAIN-NULL; IMML5 HV-1 REVERSE RANSCRIPASE; IRFH 4 RT, IRTH 6 HVF, IREVERSE HTV-1 RANSCRIPASE; IRFH 4 RANSCRIPASE; IRFH 5 RANSCRIPAN 6 RANSCRI
SEQFOL D score	CHAIN: A; TRANSCRI CHAIN; B; CHAIN; C (HEAVY C DNA (5-C	HIV-1 REV TRANSCRI CHANI: A; TRANSCRI CHAN B; CHANN B; CHANN CI (PEAVY CI DNA (5-C)	REVE HIV-1 TRAN TERM 1HAR SUBD (E.C.2	TRAN	199.34 MML TRAN	CHAI	CHAI HIV-1 TRAN
PMF S		66.0	00.1	1.00	1		1.00
Verify		-0.13	0.05	0.36			0.00
Psi Blast		8.50-98	3,4e-65	1e-59	le-59		0
END		899	551	270	571		899
STAR T AA		341	341	326	326		341
CHAI		m					∢
PDB ED		1c9r	Ihar	lmml	lmml		Irth
SEQ EQ		1454	1454	1454	1454		1454

S CHAI STAR END ND TAA AA	S CHAI STAR END NID TAA AA	TAA AA	END AA		Psi B	last	Verify	PMF	SEQFOL D score	Coumpound CHAIN: A, B; IRTH 5	PDB annotation TRANSCRIPTASE 1RTH 15
A 345 568 0	A 345 568 0	0 899	0 899	0		-0.04		1.00		HIV-I REVERSE TRANSCRIPTASE; IVRT 4 CHAIN: A, B; IVRT 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; IVRT 6 HIV-1 REVERSE TRANSCRIPTASE IVRT 15
lvrt B 345 668 0 -0.09	B 345 668 0	0 899	0 899	0		-0.09		90'1		HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B; 1VRT 5	NUCLEOTIDYL TRANSFERASE HIV-1 RT; IVRT 6 HIV-1 REVERSE TRANSCRIPTASE IVRT 15
3hvt B 342 668 3.4¢-100 -0.11	B 342 668 3.4c-100	668 3.4c-100	668 3.4c-100	3.4e-100		-0.11		99'0		NUCLEOTIDYLTRANSFERASE REVERSE TRANSCRIPTASE (E.C.2.7.7.49) 3HVT 3	
3hvt B 342 672 3.40-100	В 342 672	672	672		3.4c-100				84.10	NUCLEOTIDYLTRANSFERASE REVERSE TRANSCRIPTASE (E.C.2.7.7.49) 3HVT 3	
ldus A 6 135 5.1c-13 -0.00	A 6 135 5.1c-13	135 5.10-13	135 5.10-13	5.10-13		-0.00		-0.08		MJ0882; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII
ligi 25 94 6.8e-25 0.37	25 94 6.80-25	94 6.8e-25	94 6.8e-25	6.8e-25		0.37		00'1		GROWTH FACTOR INSULIN- LIKE GROWTH FACTOR II (IGF- II, IGF-2) 11GL 3 (NMR, 20 STRUCTURES) 11GL 4 11GL 78	
ligi 25 94 6.8 0-2 5	25 94	94	94		6.8e-25				108.25	GROWTH FACTOR INSULIN- LIKE GROWTH FACTOR II (IGF- II, IGF-2) 11GL 3 (NMR, 20 STRUCTURES) 11GL 4 11GL 78	
3lri A 16 93 4.5c-25 -0.15	A 16 93 4.5e-25	93 4.5c-25	93 4.5c-25	4.5e-25		-0.15		1.00		INSULIN-LIKE GROWTH FACTOR I; CHAIN: A;	GROWTH FACTOR INSULN-LIKE GROWTH FACTOR, I GROWTH FACTOR, I GROWTH FACTOR, INM, PROTEIN 2 STRUCTURE, DISTANCE GBOMETRY
Zocc E 46 132 6.8e-37 0.33	E 46 132 6.8e-37	132 6.8e-37	132 6.8e-37	6.8e-37	\top	0.33		1.00		CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J,	OXIDOREDUCTASE FERROCYTOCHROME C:OXYGEN

PDB annotation	OXIDOREDUCTASE; OXIDOREDUCTASE, CYTOCHROME(C)-OXYGEN, CYTOCHROME C 2 OXIDASE	OXIDOREDUCTASE FERROCYTOCHROME C'OXYGEN OXIDOREDUCTASE; CYTOCHROME(C)-OXYGEN; CYTOCHROME(C)-OXYGEN; CYTOCHROME C 2 OXIDASE	MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- ACTIVATED, TROPONIN, E-F FAND 2 CALCIUM-BINDING PROTEN	TRANSFERASE IL-2-INDUCIBLE T- CELL KINASE; TRANSFERASE; REGULATORY INTRAMOLECULAR COMPLEX, KINASE	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION	METAL BINDING PROTEIN CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, SH3 2 DOMAIN, CYTOSKELETON	
Coumpound	K, L, M, N, O, P, Q OXIII OXIII CYTY CYTY	CYTOCHROME COXIDASE; OXII CHAIN: A, B, C, D, E, F, G, H, J, J, PERR K, L, M, M, O, P, Q, OXII CYTIC CYTIC CYTIC	TROPONIN C; CHAIN: A, B; CON CON ACT ACT 2 CA	ITK; CHAIN: NULL; TRAI CELI REG ROM	ш	PSD-95; CHAIN: A; CRIPT; PEPT CHAIN: B; LOC.	SPECTRIN ALPHA CHAIN; PRO' CHAIN: A; DUP	SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 CORD A TERNANAL 1 CORD 1
SEQFOL D score		115.24						
PMF			1:00	0.29	0.87	0.92	0.54	0.13
Verify score			0.64	0.01	-0.14	0.28	-0.25	-0.16
Psi Blast		6.8e-37	00:00	3e-I1	Ie-18	3.4e-16	3e-12	4.5e-11
END		132	040	408	365	341	392	408
STAR T AA		46	109	332	248	248	334	340
CHAI N ID		н	<		¥	¥	V	V
PDB		20cc	lavs	lawj	Ib8q	1be9	1g2b	1gbr
SEQ No.		1458	1459	1459	1459	1459	1459	1459

PDB annotation					CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN	KINASE HCASK, GLGF REPEAT, DHR, PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CILUSTERING, KINASE	KINASE HCASK, GLGF REPEAT, DHS; PDZ DOMANI, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT
Coumpound	WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	ADAPTOR PROTEIN CONTAINING BEA AND SH3 GROWTH FACTOR RECEPTOR- BOUND PROTEIN 2 (RRB2) IGFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) IGFC 4	TRANSFERASE GUANYLATE KINASE (E.C.2.7.4.8) COMPLEX WITH 1GKY 3 GUANOSINE MONOPHOSPHATE 1GKY 4	TRANSFERASE GUANYLATE KINASE (E.C.2.7.4.8) COMPLEX WITH 1GKY 3 GUANOSINE MONOPHOSPHATE 1GKY 4	INTERLEUKIN 16; CHAIN: NULL;	HCASK/LIN-2 PROTEIN; CHAIN: A, B;	HCASK/LIN-2 PROTEIN; CHAIN: A, B;	HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;
SEQFOL D score			146.00					
PMF		0.66		0.1	0.95	00.1	86.0	0.96
Verify		0.36		0.80	0.31	0.19	0.07	0.19
Psi Blast		1e-10	10-68	1e-68	1.1e-16	3c-17	3.4e-16	3.4e-14
END		408	663	662	345	337	338	342
STAR T AA		349	479	480	253	254	257	253
CHAI N ID				-		٧	<	
E E		1gfe	1gky	1gky	1116	1kwa	Ikwa	1pdr
SEQ EI SO SO SO SO SO SO SO SO SO SO SO SO SO S		1459	1459	1459	1459	1459	1459	1459

	ALPHA SPECTŘÍN, CHAIN: CIRCULAR PERMUTANT PWT; NULL; DOMAIN, CYTOSKELETON	L NITRIC OXIDE (RESIDUES 1-130);	AIRANE, I SYNTROPHIN. (RESIDUSS 77-17); CHADR. A; PROTEINOXIDOREDUCTASE BETA-WIRCHOALI NITRO COLIDE SYNTHASE (RESIDUES 1-130); FINGHAN: B:	ALPHA II SPECTRIN; CHAIN: A; CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN	TEIN KINASE	SEM-5; ISBM 3 CHAPLA, AB. SIGNAL TRANSDUCTION PROTEIN ISBM 5 (JARSEDIUG PROLINE). SRCHOMOLOOY 3 (SH3) DOWAIN, RICH PRITIDE ROM MISOS. PRITIDE-BINDING PROTEIN, ISBM 8 CHAIN; C, D ISBM 109 EXCHANGE FACTOR ISBM 199 EXCHANGE FACTOR ISBM 199	ALPHA-SPECTRIN, CHAIN: CYTOSKELETON CAPPING NULL; DUPLICATION, REPEAT, 2 SH3 DOMAIN, CYTOSKELETON DOMAIN, CYTOSKELETON	TRANSFERASE URIDYLATE
-	ALPHA S NULL;	NEURONAI SYNTHASE CHAIN: A;	ALPHA-1 S (RESIDUES NEURONA SYNTHASI CHAIN: B:	ALPHAI	TYROSINE-PRO BTK; CHAIN: A;	SEM-5; II ISEM 5 1 RICH PEI ISEM 8 C	ALPHA-S NULL;	TRANSFERASE URI KINASE (E.C.2,7,4,-)
SEQFOL D score								
PMF score	0.58	96.0	00.1	0.48	0.47	0.41	0.40	69.0
Verify score	0.46	0.13	0.24	0.10	0.41	-0.10	0.22	0.10
Psi Blast	4.5e-11	1.5e-17	4.5e-16	3c-11	1.36-10	1.5e-10	6e-13	1.4e-07
END	408	362	336	408	408	408	392	629
STAR T AA	347	254	250	350	349	350	334	477
CHAI		<	Ą	4	∢	٧		
PDB CI	lpwt	Iqau	Iqav	1qkw	1qly	lsem	Itud	lukz
SEQ ID NO:	1459	1459	1459	1459	1459	1459	1459	1459

PDB annotation	PHOSPHOTRANSFERASE, TRANSFERASE		HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS, SPECIFICITY 2 OF BINDING	KINASE KINASE, PHOSPHOTRANSFERASE	TRANSFERASE ATP:DTMP PHOSPHOTRANSFERASE	HEXOKINASE ATP'.D-HEXOSE-6- PHOSPHOTRANSFERASE; HEXOKINASE; PHOSPHOTRANSFERASE	HEXOKINASE ATP/:D-HEXOSE-6- PHOSPHOTRANSFERASE; HEXOKINASE; PHOSPHOTRANSFERASE	TRANSFERASE STRUCTURALLY HOMOLOGOUS DOMAINS	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA	SERINE PROTEINASE TRYPSIN-LIKE
Coumpound	A, B;	TRANSFERASE(PHOSPHOTRA NSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	THYMIDYLATE KINASE; CHAIN: A, B, C, D, E, F, G, H;	THYMIDYLATE KINASE; CHAIN: A;	HEXOKINASE; CHAIN: A, B;	HEXOKINASE; CHAIN: A, B;	HEXOKINASE TYPE I; CHAIN: N;	TRYPSIN; CHAIN: A, B, C, D;	TRYPSIN; CHAIN: A, B, C, D;	BETA-TRYPTASE; CHAIN: A, B, C, D;	BETA-TRYPTASE; CHAIN: A, B,
SEQFOL D score							459.01			104.84		00'16
PMF		0.98	1:00	9.04	61.0	1:00		1.00	00'1		1.00	
Verify		0.12	0.32	0.28	-0.03	1.13		1.07	0.88		0.50	
Psi Blast		96-96	1.5e-13	9e-10	7.5e-16	0	0	0	1.46-80	1.4e-80	1.7e-74	1.7e-74
END		995	332	995	999	498	499	201	239	239	233	239
STAR T AA		475	253	479	478	_	_		30	30	30	30
CHAI N ID			٧	S	Ą	∢	<	z	<	∀	<	Ą
FDB ID		3adk	3pdz	3tmk	4tmk	1bg3	16g3	lcza	1a0j	la0j	1a0I	la0l
SEQ UD NO:		1459	1459	1459	1459	1461	1461	1461	1464	1464	1464	1464

PDB annotation	SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, ZYMOGEN, 2 SIGNAL, MULTIGENE FAMILY	HYDROLASE (SERINE PROTEASE) MYELOBLASTIN; HYDROLASE, SERINE PROTEASE, GLYCOPROTEIN, ZYMOGEN, SIGNAL			
Coumpound	C, D;	ELASTASE; CHAIN: P;	ELASTASE; CHAIN: P;	TRYPSIN; CHAIN: NULL;	PR3; CHAIN: A, B, C, D;	COMPLEX(PROTEINASE/INHIB ITOR) TRYPSIN (E.C.34.21.4) COMPLEXED WITH INHIBITOR FROM BITTER IMCT 3 GOURD IMCT 4	COMPLEX(PROTEINASE/INHIB ITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER IMCT 3 GOURD IMCT 4	PROTEGLASEERINE PROTEGLASE, HUMAN ELICOCYTE BLASTASE (HLE) (HUE)) IPPF 3 (E.C.3.4.1.37) COMPLEX WITH THE THIRD DOMAIN OF TURKEY IPPF 4 (OMITIVE) IPPF 5
SEQFOL D score			115.93	98.94	200.42		103.86	315.52
PMF		1.00				00.1		
Verify		0.64				0.74		
Psi Blast		1.7e-75	1.7e-75	1.7e-79	6e-71	8.5e-83	8.5e-83	1e-65
END		239	239	239	237	239	239	237
STAR T AA		30	30	30	30	30	30	30
CHAI		Ь	d.		<	<	∢	ш
PDB ID		1bru	1bru	Idpo	<u>1</u> 2	Imct	Imct	lppf
SEQ NO ID		1464	1464	1464	1464	1464	1464	1464

Stop PDB GRA STAR EAD PAB Blast Verify PMF SEOPOL Coumpound PDB annountion PDB announties PDB annou							
PDB CHA STAR END Pal Blast Verify PMF SEQPOL	PDB annotation	HYDROLASE MICROFLASMINOGEN, SERINE PROTEASE, ZYMOGEN, PHYDROLYSEN 2 FAMILY, HYDROLASE	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERNE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)	COMPLEX (SERINE PROTEASEMHEIDOR) TRYPSIN INHEITOR, SCHELEX, METAL, BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE SUBSTRATE INTERACTIONS, 3		
PDB CIAA STAR END Pa Blast Verify PMF	Coumpound	PLASMINOGEN; CHAIN: A, B, C, D;	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	ECOTIN, CHAIN: A; ANIONIC TRYPSIN, CHAIN: B;	PROGENIES (ERRINE PROTEINASE) TRYPSIN CCA, 34,14 (COMPLEXED WITH THE INVESTION LITRN 3 DISCOPROPYL ELOROPHOREAD PROLEDIANA E (DPP) ITRN 4 HUMAN TRYPSIN, DPP INHIBITED ITRN 6	HYDROLASE (SERINE PROTEINASE) TRYPSIN
PDB CHAM STAR END Pd Blast Verify	SEQFOL D score	117.30		97.78			100.94
PDB CHAN STAR END Pd Blast Pd Blast Pd TAA AA Pd Pd Pd Pd Pd Pd	PMF		00.1		1.00	1.00	
PDB CIAA STAR END FAA AA FAA FAA	Verify		0.65		0.45	0.79	
1918 Cital STAR EVD 110 N 110 T T AA AA AA 122 1239 Cital Psi Blast	3.4e-71	3.4e-72	3.46-72	1.7e-78	5.1e-80	5.1e-80	
100 100	END	239	239		239	239	240
1908 1917 1918 1818 1818 1111 1111 1111 111	STAR T AA	12	30	30	30	30	30
	CHAI	∢	Đ	Ð	м	∢	4
	PDB ID	Iqrz	lsgf	lsgf	Islw	<u> </u>	Itm
	SEQ NO.	1464		1464	1464	1464	1464

							_		_
PDB annotation				SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL	SIGNAL TRANSDUCTION SIGNAL TRANSDUCTION	SIGNAL TRANSDUCTION SIGNAL TRANSDUCTION	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX, 14-3-3, PHOSPHOPEPTIDE, SIGNAL TRANSDICTION	COMPLEX (SIGNAL
Coumpound	(E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR 1TRN 3 DIISOPROPYL FLUOROPHOSPHOFLUORIDAT E (DPP) 1TRN 4 HUMAN TRYPSIN, DPP INHIBITED 1TRN TRYPSIN, DPP INHIBITED 1TRN TRYPSIN, DPP INHIBITED 1TRN	HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE NHIBITOR 2TBS 3	HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS 3	BETA TRYPSIN; CHAIN: NULL;	BETA TRYPSIN; CHAIN: NULL;	14-3-3 PROTEIN ZETA; CHAIN: A, B, C, D;	14-3-3 PROTEIN ZETA; CHAIN: A. B. C. D;	14-3-3 PROTEIN ZETA; CHAIN: A, B; PHOSPHOPEPTIDE; CHAIN: Q, R	14-3-3 PROTEIN ZETA; CHAIN:
SEQFOL D score		,	97.32		99.14	234.97			284.35
PMF		1.00		1.00			00.1	00.I	
Verify score		0.65		0.73			0.55	0.59	
Psi Blast		5.1e-79	5.1e-79	1.7e-76	1.7e-76	1.7e-98	1.7e-98	0	0
END		237	239	239	239	229	230	232	232
STAR		30	30	30	30	23	3	e	3
CHAI N ID						4	¥	∢	Ą
PDB CI		2tbs	2fbs	5ptp	5ptp	la4o	1a4o	1qja	Iqja
SEQ NO:		1464	1464	1464	1464	1470	1470	1470	1470 Iqja

PDB annotation	TRANSDUCTION/PEPTIDE) COMPLEX, 14-3-3, PHOSPHOPEPTIDE, SIGNAL TRANSDUCTION	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION	TRANSMEMBRANE 2 PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22	TANDEM 3-HELLX COLLED-COLLS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22 TANDEM 3-HELIX COLLED-COLLS	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELLY COLLED-COLLS, STRUCTURAL PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35	KDA PROTEIN, P35A, THREE HELIX BUNDLE	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN P25A THREE HELIY	BUNDLE	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL,
Coumpound	A, B; PHOSPHOPEPTIDE; CHAIN: Q, R	COLICIN IA; CHAIN: NULL;		ALPHA SPECTRIN; CHAIN: A, B, C;		ALPHA SPECTRIN; CHAIN: A, B, C;			ALPHA SPECTRIN; CHAIN: A, B. C:			SYNTAXIN-1A; CHAIN: A, B, C;		SYNTAXIN-1A; CHAIN: A, B, C;			HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;
SEQFOL D score		133.38															
PMF				0.03		-0.17			0.39			-0.13		-0.15			0.11
Verify score				-0.15		0.12			0.05			0.19		0.01			0.02
Psi Blast		3.4e-08		6e-15		7.5e-16			3e-20			1.5e-09		4.5e-08			66-19
END		621		322		363			248			139		214		_	426
STAR T AA		48		117		152			38			23		56		_	196
CHAI N ID				∢		<			A			٧		4			¥
PDB		lcii		lcm		lcm			lcnn			lez3		lez3			Idun
SEQ NO: D		1471		1471		1471			1471			1471		1471			1471

			_						_	_				_				_				_			_
PDB annotation	CONTRACTILE PROTEIN CONTRACTILE PROTEIN TRIPLE- HELLY COLLED COLL	CONTRACTILE PROTEIN	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE	SIGMA FACTOR, TRANSCRIPTION REGULATION	LEGAMENT AND A LANGE LANGE AND A LOCAL DESCRIPTION AND	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	KEGULATION/ANK KEFEAT), ANKYRIN 2 REPEAT HELIX		STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	STRICTIRAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN AT PHA	HELICAL LINKER REGION, 22	I AINDEM 3-FIELTA COLLEGI-COLLS,
Coumpound	HUMAN SKELETAL MUSCLE AI PHA ACTININ 2: CHAIN: A:	ALL INCREMENTS, CHAINER,	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;		O THE TAX OF THE PARTY OF THE P	NF-KAPPA-B P05; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	. Y		ALPHA SPECTRIN; CHAIN: A,	в, с;			ALPHA SPECTRIN: CHAIN: A.	B,C;			AT PHA SPECTRIN: CHAIN: A	B, C,				ALPHA SPECTRIN; CHAIN: A, B. C:		
SEQFOL D score																									
PMF	-0.02		0.03			0.0				0.15				0.19				0.55					0.35		
Verify	60:0		-0.11			-0.56				-0.18				-0.12				-0.05	1				0.19		
Psi Blast	1.5e-15		60-ay		27000	0.0045				3e-06				9e-13				1 50-15					4.5e-15		
END	487		307			:				337				458				687					724		
STAR	217		32		-	3				150				241				460					200		
CHAI N ID	A				1	a)				۷				4				4					∢		
PDB	Iqua		lsig			<u> </u>				lcun				lcun				lenn					lenn		
SEQ NO. ID	1471		1471		10,	C/ +				1476				1476				1476					1476		

PDB annotation	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	ENDOCYTOSIS/EXOCYTOSIS	NSEC1; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS	NSEC1; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS	NSECI; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS	NSEC1; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN ASSOCIATED 35	KDA PROTEIN, P35A, THREE HELIX	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN ASSOCIATED 35
Coumpound		ALPHA SPECTRIN; CHAIN: A,	в, с;				ALPHA SPECTRIN; CHAIN: A,	ည်း				ALPHA SPECTRIN; CHAIN: A,	B,C;				SYNTAXIN BINDING PROTEIN	I; CHAIN: A; SYNTAXIN 1A;	CHAIN: B;	SYNTAXIN BINDING PROTEIN	1; CHAIN: A; SYNTAXIN 1A;	CHAIN: B;	SYNTAXIN BINDING PROTEIN	I; CHAIN: A; SYNTAXIN IA;	CHAIN: B;	SYNTAXIN BINDING PROTEIN	I; CHAIN: A; SYNTAXIN IA;	CHAIN: B;	SYNTAXIN-1A; CHAIN: A, B, C;			SYNTAXIN-1A; CHAIN: A, B, C;	
SEQFOL D score																																	
PMF		0.42					0.09					-0.14					-0.05			0.01			90.0			0.03			0.03			-0.06	
Verify		0.15					80.0					-0.00					0.03			-0.30			-0.21			-0.19			-0.26			0.00	
Psi Blast		9e-17					1.2e-13					6e-12					6e-16			1.5e-16			6e-18			6e-13			3e-07			1.5e-11	
END		794					820					916					423			262			711			116			363			612	
STAR T AA		583					632					721					216			380			503			700			526			593	
CHAI N ID		٧					٧					¥					В			В			м			В			٧			V	
FDB		1cun					lcun					lcnn					ldnl			Idhi			ldnl			Idu]			lez3			lez3	
SEQ NO:		1476					1476					1476					1476			1476			1476			1476			1476			1476	

	S HELIX	S VTED 35 S HELLIX	K HELIX	KOTEIN	PLE-	IPLE-	PLE-	IPLE-			AIN, NDING	AIN, INDING
PDB annotation	KDA PROTEIN, P35A, THREE HELIX BUNDLE	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	CHAPERONE ARCHAEAL PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELLX COLLED COIL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN			IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD, RNA-BIND	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD, RNA-BINDING
		i: A, B, C;	4: A;	280	IUSCLE IAIN: A;	USCLE IAIN: A;	USCLE IAIN: A;	USCLE IAIN: A;	S) SERYL- TRNA LEXBD XAMATE-		CHAIN:	CHAIN:
Coumpound		1A; CHAIN	EIN; CHAIP	CHAIN: A	ELETAL M TININ 2; CF	ELETAL M FININ 2; CI	ELETAL M TININ 2; CF	ELETAL M TNIN 2; CE	NTHETASE HETASE SERINE- ES 3 COMP		COLOGICA	COLOGICA
ŭ		SYNTAXIN-1A; CHAIN: A, B, C;	SSO1 PROTEIN; CHAIN: A;	PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	LIGASE(SYNTHETASE) SERYL- TRNA SYNTHETASE (E.C.6.11.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE- AMP 1SES 4		NEURO-ONCOLOGICAL	NEURO-ONCOLOGICAL VENTRAL ANTIGEN I; CHAIN:			
SEQFOL D score												
PMF		0.19	0.15	0.59	0.00	90.0	0.54	0.21	0.12		0.82	0.82
Verify	-	0.28	0.17	-0.29	-0.19	-0.29	-0.02	0.07	-0.07		0.62	0.62
Psi Blast		4.5e-10	9e-10	0.0001	4.5e-22	3e-26	6e-24	1.5e-24	0.00017		0.00015	0.00015
END AA		822	849	711	573	640	749	790	555		299	199
STAR		704	491	548	320	390	480	528	464		609	609
CHAI N ID		<	4	U	∢	4	4	¥.	¥		A	∢
PDB		lez3	Iţ	Ifxk	lquu	lquu	lquu	Idun	1ses		1dt4	1dt4
SEQ ID NO:		1476	1476	1476	1476	1476	1476	1476	1476	ľ	1479	1479

			r				
PDB annotation	ALPHA-BETA FOLD RNA-BINDING MOTIF	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD RNA-BINDING MOTIF	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD RNA-BINDING MOTIF	POLYRIBONUCLEOTIDE TRANSBERASE DOLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, AFP-GTP 2 DIPHOSPHOTRANSFERASE, RNA PROCESSING, RNA DEGRADATION	POLYRIBONÚCLEOTIDE TRANSBERAGE POLYNUCLEOTIDE PHOSPHORYLASE, QUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-CIP DIPHOSPHOTRANSFERASE, 2RNA PROCESSING, RNA DEGRADATION	RNA BINDING PROTEIN/RNA ASTROCYTIC NOVA-LIGE RNA- BINDING PROTEIN; KH DOWAIN, ALPHA-BETA FOLD, RNA-BINDING MOTTE, ROTEIN/RNA 2 STRUCTURE	RNA BINDING PROTEIN KH3; HNRNP K, KH DOMAIN, THREE- DIMENSIONAL STRUCTURE, NMR,
Coumpound	NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	RNA-BINDING NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	RNA-BINDING NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	GUANOSINE PENTAPHOSPHATE SYNTHETASE, CHAIN: A;	GUANOSINE PENTAPHOSPHATE SYNTHETASE, CHAIN: A;	RNA-BINDING PROTEIN NOVA-2; CHAIN: A, B; 20-MER RNA HAIRPIN; CHAIN: C, D;	HNRNP K; CHAIN: A;
SEQFOL D score							
PMF		0.94	. 68.0	1.00	1.00	0.72	0.36
Verify score		0.59	09'0	0.75	0.49	0.50	0.36
Psi Blast		3e-06	1e-05	0	0	0.00014	0.0014
END AA		299	299	613	739	91.9	129
STAR T AA		609	609	51	51	609	019
CHAI N ID		ပ	Q	∢	∢	¥	V
PDB CI		1dtj	146	1e3h	le3p	lec6	1khm
S B SE		1479	1479	1479	1479	1479	1479

PDB annotation	C-MYC, 2 DIPOLAR COUPLING, DNA-BINDING, RNA-BINDING, RNA BINDING 3 PROTEIN	SI RNA-BINDING DOMAIN POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE, SI RNA-BINDING DOMAIN, POLYNUCLEOTIDE PHOSPHORYLASE 2 [PWASE)	RIBONUCLEOPROTEIN RNA- BINDING PROTEIN IVIG 19	GENE REGULATION APO PROTEIN	GENE REGULATION APO PROTEIN	CELL CYCLE CDC6P; CDC6, CDC18, ORC1, AAA PROTEIN, DNA REPLICATION INITATION 2 FACTOR, CELL CYCLE CONTROL FACTOR.	HELICASE DNA REPAIR, DNA REPLICATION, SOS RESPONSE, HELICASE, ATP- 2 BINDING, DNA- BINDING	ACTIN-BINDING PROTEIN ACTIN- BINDING PROTEIN, CALCIUM- BINDING, PHOSPHORYLATION	STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR DYSTROPHY, CALPONIN HOMOLOGY DOMAIN, 2 ACTIN- BINDING, UTROPHIN
Coumpound		PNPASE; CHAIN: NULL;	VIGILIN; IVIG 5 CHAIN: NULL; IVIG 6	EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN; A;	EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	CELL DIVISION CONTROL PROTEIN 6; CHAIN: A, B;	PCRA (SUBUNIT); CHAIN: A; PCRA (SUBUNIT); CHAIN: B; PCRA (SUBUNIT); CHAIN: C; PCRA (SUBUNIT); CHAIN: D;	T-FIMBRIN; CHAIN: NULL;	Dystrophin; Chain: A, B, C, D;
SEQFOL D score									
PMF		0.1	0:30	0.00	0.03	0.54	0.83	96'0	0.68
Verify		0.78	0.46	-0.14	-0.21	-0.14	-0.19	0.28	0.54
Psi Blast		5.1e-21	1e-06	1.7e-06	6000	0.00015	1.5e-11	6.8e-26	5.1e-28
END		751	299	528	209	492	524	122	120
STAR T AA		675	603	442	447	427	444	4	7
CHAI				<	¥	∢	V.		<
EDB CI		lsro	Ivig	x6p1	х6р[lfiin	1qhg	Iaoa	Idxx
SEQ B B S		1479	1479	1480	1480	1480	1480	1484	1484

PDB annotation	STRUCTURAL PROTEIN CALPONIN HOVOLOGY DOMAIN, DOMAIN SWAPFING, ACTIN BINDING, 2 UTROPHIN, DYSTROPHIN, STRUCTURAL PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC PINGER PROTEIN	COMPLEX (DNA-BINDING PROTEINDNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION		LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,	METAL BINDING PROTEIN RING FINGER PROTEIN MATT: RING
Coumpound	UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;	TFIIIA, CHAIN: A, D; 58 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	TRANSCRIPTION FACTOR PML; CHAIN: NULL;	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	SIGNAL TRANSDUCTION PROTEIN CBL; CHARN; A; ZAP- 70 PEPTIDE; CHARN; B; UBIQUITIN-COMUGATING ENZYME E12-18 KDA UBCH7; CHARN; C;	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI;
SEQFOL D score							
PMF	0.39	0.01	0.41	0.00	0.29	0.15	0.62
Verify	0.33	-0.10	0.08	-0.38	-0.35	-0.24	0.26
Psi Blast	3.4e-26	0.0045	0.00045	0.0001	3.4c-10	5.1c-09	5.1c-06
END	121	953	926	377	378	381	387
STAR T AA	5	998	873	339	336	336	336
CHAI N ID	٧	V	V			٧	<
80g El	lqag	1116	2gli	lbor	lche	1fbv	1g25
SEQ B G	1484	1486	1486	1487	1487	1487	1487

PDB annotation	FINGER (C3HC4)	DNA-BINDING PROTEIN VID) RECOMBINATION ACTIVATING PROTEIN I, RAGI, VID) RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINGLEAR GLUSTER, ZINC FINGER, LOSTER, ZINC FINGER, DAVA-BINDING PROTEIN	HEXAMERIZATION DOMAIN HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT	CHAPERONE HSLV; HSLU	CHAPERONE, HSLVU, CLPQY, AAA-	PROTEOLYSIS, PROTEASOME	F	CHAPERONE, HSLVU, CLPQY, AAA-	PROTEOLYSIS, PROTEASOME	HYDROLASE ARSA ATPASE; P.	LOOP, ANTIMONITE BINDING SITE, ATP BINDING SITE	CELL CYCLE CDC6P; CDC6, CDC18,	ORC1, AAA PROTEIN, DNA	REPLICATION INITATION 2	FACTOR, CELL CYCLE CONTROL FACTOR	CHAPERONE AAA-ATPASE, CLPY,	ATP-DEPENDENT PROTEOLYSIS	-	ATP-DEPENDENT PROTEOLYSIS	TRANSFERASE SHIKIMATE KINASE, PHOSPHORYL TRANSFER, ADP.
· Coumpound	CHAIN: A;	RAGI; CHAIN: NULL;	N-ETHYLMALEIMIDE- SENSITIVE FUSION PROTEIN; CHAIN: A;	HEAT SHOCK PROTEIN HSLV;	CHAIN: A, B, C, D; HEAT	CHAIN: E, F;	HEAT SHOCK PROTEIN HSLV;	CHAIN: A, B, C, D; HEAT	CHAIN: E. F.	ARSENITE-TRANSLOCATING	ATPASE; CHAIN: A;	CELL DIVISION CONTROL	PROTEIN 6; CHAIN: A, B;			HEAT SHOCK PROTEIN HSLU;	CHAIN: A;	HEAT SHOCK PROTEIN HSLU;	CHAIN: A;	SHIKIMATE KINASE; CHAIN: A, B;
SEQFOL D score																				
PMF		0.06	0.18	-0.13			0.05			0.28		0.45				950		0.04	9	0.49
Verify score		0.10	0.11	10.0			-0.20			-0.39		0.15				0.46		-0.11	02.0	-0.53
Psi Blast		3.4e-09	1.2e-11	8.5e-12			1.5e-12			0.0015		1.2e-15				1.2e-37		1.2e-17		1.56-05
END		387	782	434			634			514		679				599		819	200	969
STAR		320	929	339			339			82		344				330		339	2,0	309
CHAI			<	Э			Э			Ą		٧				Ą		∢		٧
PDB		Irmd	1d2n	1e94			1e94			1f48		Ifun				1g41		1g41	Tabl.	ISDK
S e S		1487	1490	1490			1490			1490		1490				1490		1490	1,400	1490

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PDB annotation	SHIKIMATE 2 PATHWAY, P-LOOP PROTEIN, TRANSFERASE	PROTEIN TRANSFORT FIFTY-FOUR HOMOLOG, PM; FFEI, SRF94, STONAL RECOGNITION PARTICLE, GTPASE, M DOMANT, 2 RNA-BINDING, SIGNAL SEQUENCE-BINDING, HELK-TURN-HELLX, 3 PROTEIN TARGETING, PROTEIN TRANSFORT	COMPLEX (INHIBITORAUCI EASE) COMPLEX (INHIBITORAUCI EASE) COMPLEX (INHIBITORAUCI EASE) COMPLEX (INHIBITORAUCI EASE) MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	RANGERPITON RALP, RANGER, GPASE-ACTIVATING ROCHEIN FOR SHI, GTPASE-ACTIVATING PROTEN, GAR, RNATE, RANGAR, LRO, LEICURE-2 RICH REPRAT PROTEIN, VENNING, HEMIEDRA, TWINNING, HEMIEDRA, TWINNING, MREOGERAL TWINNING,	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS		PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
Coumpound		FFH; CHAIN: A, B, C;	RIBONUCLEASE INHBITOR; CHAIN: A, D, ANGIOGENIN; CHAIN: B, E;	PROTENENCIJALING PROTENENA, SCHPO, CHAIN: A, B;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;		LITHOSTATHINE; CHAIN: NULL
SEQFOL D score							
PMF		0.01	0.94	81.0	9.65		1.00
Verify		-0.24	0.10	0.03	0.33		0.82
Psi Blast		16-05	1.5e-48	6.8e-27	3.4e-43		le-42
END		537	394	391	393		166
STAR T AA		347	178	178	178		36
CHAI N ID		<	<	. ·			
FDB		2ffh	la4y	Тутв	2bnh		Ilit
SEQ NO:		1490	1491	1491	1491		1495

PDB annotation	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE	PROTEIN TRANSPORT HELIX- TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT	HYDROLASE SERCAI; ION PUMP, CALCIUM, MEMBRANE PROTEIN, P. TYPE ATPASE, ACTIVE 2 TRANSPORT	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2 HYPERTHERMOSTABLE PROTEIN	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC,
Coumpound	LITHOSTATHINE; CHAIN: NULL	LITHOSTATHINE; CHAIN: NULL	LITHOSTATHINE; CHAIN: A;	LITHOSTATHINE; CHAIN: A;	LITHOSTATHINE; CHAIN: A;	VESICULAR TRANSPORT PROTEIN SEC17; CHAIN; A;	CALCHUM-TRANSPORTING ATPASE SARCOPLASMIC CHAIN: A;	DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB;
SEQFOL D score		212.11			226.04				
PMF	1.00		1.00	1.00		-0.17	0.46	96.0	0.83
Verify	0.82		0.77	0.77		0.14	-0.16	0.20	-0.10
Psi Blast	7.5e-43	7.5e-43	1e-44	6c-47	6e-47	1.1e-13	0	le-12	1.4e-19
END	991	166	166	991	991	634	713	540	516
STAR T AA	36	36	23	23	23	489	_	393	448
CHAI N ID			<	<	٧	V	<	4	4
EDB ED	Ħ	Ħ	lqdd	Iqdd	lqdd	1qqe	leul	lc40	1c40
SEQ NO:	1495	1495	1495	1495	1495	1497	1498	1499	1499

PDB annotation	HELICASE, 2 HYPERTHERMOSTABLE PROTEIN	HYDROLASE UVRB; MULTIDOMAIN PROTEIN	HYDROLASE UVRB; MULTIDOMAIN PROTEIN	GENE REGULATION APO PROTEIN	GENE REGULATION APO PROTEIN	TRANSLATION YEAST INITIATION FACTOR 4A, EIF4A; HELICASE, INITIATION FACTOR 4A DEAD-BOX	PROTEIN	TRANSLATION EUKARYOTIC INITIATION FACTOR 44; IF44, HELICASE, DEAD-BOX PROTEIN	TRANSLATION BUKARYOTIC INITIATION FACTOR 4A; 1F4A, HELICASE, DEAD-BOX PROTEIN	HELICASE HELICASE, RNA, HEPATITIS, HCV, ATPASE, NTPASE	GENE REGULATION EIF44; TRANSLATION INTIATION, SACCHAROMYCES CEREVISIAE, DEAD BOX 2 PROTEIN FAMILY	HELICASE, HEPATITIS C VIRUS, HCV, UNWINDING MECHANISM	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN; 2 CALCIUM- BINDING PROTEIN
-	HH		$\overline{}$	-	-		PRC	医医医	京国田	田田	SAC TRA		CAL
Coumpound	CHAIN: A;	EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	BUKAR YOTIC INITIATION FACTOR 4A; CHAIN: A;		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	YEAST INITIATION FACTOR 4A; CHAIN: A, B;	HCV HELICASE; CHAIN: A, B;	TRANSLATION INITIATION FACTOR 4A; CHAIN: A;	RNA HELICASE; CHAIN: NULL	PROTEIN KINASE C (BETA); CHAIN: A, B;
SEQFOL D score													77.04
PMF		61.0	0.80	60.0	0.76	0.86		1.00	1.00	0.22	1.00	0.04	
Verify score		-0.57	0.17	-0.16	65.0	0.26		0.83	0.47	-0.18	0.55	-0.59	
Psi Blast		89000'0	8.5e-13	9e-29	3.4e-16	1.2e-43		3.4e-59	0	0.0003	5.1e-56	1.5e-53	9e-25
END		223	240	531	528	558		340	558	325	340	522	137
STAR		144	393	258	380	376		127	127	158	127	158	12
CHAI N ID		A	٧	A	٧	¥		A	8	٧	¥		A
FDB TD		1d2m	1d2m	149x	149x	Ifuk		Ifou	Ifon	lhei	lqde	8ohm	1a25
SEQ NO.		1499	1499	1499	1499	1499		1499	1499	1499	1499	1499	1502

PDB annotation	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCTUM-BINDING PROTEIN CALB; CALCTUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCTUM- BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE	LIPID DEGRADATION PLC-DI; PHOSPHORAC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOI IPASE C. 3
Coumpound	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	SYNAPTOTAGMIN I; CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;
SEQFOL D score								
PMF	0.54	1.00	06.0	0.35	0.10	0.65	0.45	0.24
Verify	-0.05	0.42	0.62	0.04	0.36	0.07	0.29	0.34
Psi Blast	1.5e-26	9e-25	1.4e-24	3.4e-30	1.7e-28	1.3e-29	7.5e-24	3.4e-22
END AA	287	131	117	287	122	338	184	302
STAR T AA	167	11	88	167	19	184	22	183
CHAI N ID	V	Ą	<	A	A	٧	4	4
PDB ID	1a25	1a25	1a25	Ibyn	Ibyn	lcjy	Icjy	x(pt
SEQ B io	1502	1502	1502	1502	1502	1502	1502	1502

PDB annotation	PHOSPHOINOSITIDE-SPECIFIC	FIC LIPID DEGRADATION PLC-DI; : A, PHOSPHORIC DIESTER	_	DEGRADATION, 2 TRANSDUCER,	CALCIUM-BINDING,	PHOSPHOINOSITIDE-SPECIFIC		_	HYDROLASE, HYDROLASE, LIPID	DEGRADATION, 2 TRANSDUCER,	CALCIUM-BINDING,	PHOSPHOLIPASE C, 3	THOSPHOLNOSI I DE-SPECIFIC		CAI CHIMERINDING 2 PROTEIN	PHOSPHATIDYLSERINE, PROTEIN	KINASEC		PHOSPHOLIPID BINDING PROTEIN,	CALCIUM-BINDING 2 PROTEIN,	PHOSPHATIDYLSERINE, PROTEIN	KINASE C	Г	PHOSPHOLIPID BINDING PROTEIN,	CALCIUM-BINDING 2 PROTEIN,	PHOSPHATIDYLSERINE, PROTEIN	7	N: HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB	DOMAIN	N- HYDROLASE CATR DOMAIN.
Coumpound		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A,	B;				PHOSPHOINOSITIDE-SPECIFIC	PHOSPHOLIPASE C, CHAIN: A,	á				ALIGUE O GOLDANIA SERVICE	TYPE CHAIN A.	I IFE, CHAIN, A,			PROTEIN KINASE C, ALPHA	TYPE; CHAIN: A;	_			PROTEIN KINASE C, ALPHA	TYPE; CHAIN: A;				PHOSPHOLIPASE A2; CHAIN: NULL:		PHOSPHOLIPASE A2: CHAIN:
SEQFOL D score																														51.76
PMF score		0.16					0.21						8	3				0.07					0.88					0.28		
Verify score		0.49					0.20						02.0	70:0				-0.13					0.47					0.17		
Psi Blast		6.8e-23					3.4e-22						7-04	10-54				5.1e-28					6.8e-27					6e-23		4.5e-25
END		121					302						107	ć				295					117				1	276		145
STAR		27					183						2	-				183					18				, , ,	184		20
CHAI		V					m							¢				Ą					٧							
PDB		Idjx					Idjx				_		140	ćen i				Idsy					Idsy					ırlw		Irlw
SEQ NO.		1502					1502						1200	1007				1502					1502				0000	1502		1502

	, CALB	AIN; 4, CALB				SIS C2-	SIS BETA N, C2	ON PALPHA; -BINDING, S DOMAIN,	NO
PDB annotation	HYDROLASE, C2 DOMAIN, CALB DOMAIN	HYDROLASE, C2 DOMAIN, DOMAIN, DOMAIN, CALB DOMAIN				ENDOCYTOSIS/EXOCYTOSIS C2- DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN	COMPLEX (TRANSCRIPTION REGULATION/DANA) GABBALPHA; GABBETAI; COMPLEX (TRANSCRIPTION) REGULATION/DANA) DIVA-BINDING, STUCLEAR REOTEN, ETS DOMAIN, ANKYTRI REPERTS.	1-
Coumpound	NULL;	PHOSPHOLIPASE A2; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	RABPHILIN 3-A; CHAIN: A;	SYNAPTOTAGMIN III; CHAIN: A;	GA BINDING PROTEIN ALPHA; CARIN A; OB BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, B;	GA BINDING PROTEIN ALPHA:
SEQFOL D score					59.11				
PMF		0.93	0.48	0.21		0.34	0.19	1.00	96.0
Verify		0.78	0.18	0.36		0.00	-0.57	0.40	0.29
Psi Blast		4.5e-25	3.4e-30	1.7c-28	1.7e-28	1.2e-26	6.8e-53	1.5e-26	1.2e-29
END		143	284	122	130	294	223	861	828
STAR T AA		30	167	61	2	168	144	693	694
CHAI						¥		m	ш
PDB TD		Irlw	lrsy	Irsy	Irsy	3rpb		lawc	lawc
SEQ ID	Ö	1502	1502	1502	1502	1502	1502	1503	1503

	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
								CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA: CHAIN: D. E:	REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION
									REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,
									ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
В		748	895	5.1e-38	89.0	1.00		GA BINDING PROTEIN ALPHA;	COMPLEX (TRANSCRIPTION
								PROTEIN BETA 1; CHAIN: B;	GABPBETAI; COMPLEX
								DNA; CHAIN: D, E;	(TRANSCRIPTION
									REGULATION/DNA), DNA-BINDING,
									ANKYRIN REPEATS,
m		4179	936	7.5e-34	0.72	1.00		GA BINDING PROTEIN ALPHA;	COMPLEX (TRANSCRIPTION
								CHAIN: A; GA BINDING	REGULATION/DNA) GABPALPHA;
								PROTEIN BETA I; CHAIN: B;	GABPBETAI; COMPLEX
								DIVA; CITAIN: D, E;	(IKANSCKIPIION
									REGULATION DNA, DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,
									ANKYRIN REPEATS,
	I								TRANSCRIPTION 3 FACTOR
В		780	026	1.2e-31	0.02	0.78		GA BINDING PROTEIN ALPHA;	COMPLEX (TRANSCRIPTION
								PROTEIN BETA 1: CHAIN: B:	REGULATION/DNA) GABRALFRA;
								DNA: CHAIN: D. E.	CIRANSCRIPTION
									REGULATION/DNA), DNA-BINDING,
									2 NUCLEAR PROTEIN, ETS DOMAIN,
									ANKYKIN KEPEAIS, TP ANSCRIPTION 3 FACTOR
В		847	1005	3.4e-29	80.0	-0.11		GA BINDING PROTEIN ALPHA;	COMPLEX (TRANSCRIPTION
								CHAIN: A; GA BINDING	REGULATION/DNA) GABPALPHA;
ı								PROTEIN BETA 1; CHAIN: B;	GABPBETA1; COMPLEX

PDB annotation	(TRANSCRIPTION RECULATIONDNA, DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GARBBETA!; COMPLEX (TRANSCRIPTION ECCLIFICATION/DNA), DNA-BINDING, BEGULATION/DNA), DNA-BINDING, ANCYREN REPEATS, ANCYREN REPEATS, ANCYREN REPEATS, TRANSCRIPTION 3 PACTOR	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	COMPLEX (INHERTOR PROTEIN/KICHANE) INHEITOR PROTEIN/CYCLIA-DEPENDENT KINANE, CELL CYCLE 2 CONTROL, ALPHABETA, COMPLEX INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/CRASE) FUBLIBITOR PROTEIN, CYCLIA-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHABETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT
Coumpound	DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL D score							
PMF		II 0	0.98	1.00	0.99	0.76	1.00
Verify score		0.05	0.26	09.0	0.37	0.07	0.64
Psi Blast		I.7e-29	3.4e-26	4.5e-32	I.1e-26	1.4e-24	7.5e-33
END		1045	862	937	898	862	941
STAR		. 088	269	776	695	697	61.1
CHAI		щ			В	В	В .
PDB OI		Iawc	1bd8	1548	Ibix	Iblx	1blx
S a S		1503	1503	1503	1503	1503	1503

PDB CHAI STAR END PSIBIST Verily PMF ID NID TAA AA score score	STAR END Psi Blast Verify PMF TAA AA score score	END Psi Blast Verify PMF AA score score	Psi Blast Verify PMF score score	PMF		L	SEQFOL D score	Coumpound	PDB annotation
									KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
lbu9 A 697 867 3.4e-31 0.42 0.84	867 3.40-31 0.42	3.4e-31 0.42	0.42		0.84			CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
lbu9 A, 748 894 6.8e-32 0.39 0.99	894 6.8e-32 0.39	6.8e-32 0.39	0.39		0.99			CYCLIN-DEPENDENT KINASE 6 INFIBITOR; CHAIN: A;	HORMONEGROWTH FACTOR PIB- NEAC; CELL CYCLE INHIBITOR, PI BINKAC, TUMOR, SUPRESSOR, CYCLIN- 2 DEPENDENT KINASF, HORMONEGROWTH FACTOR
1d9s A 693 833 3e-19 0.23 0.77	833 3e-19 0.23	3e-19 0.23	0.23		0.77			CYCLIN-DEPENDENT KINASE 4 INFIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT
Id9s A 776 909 1.2e-32 0.81 1.00	909 1.2e-32 0.81	L2e-32 0.81	0.81		1.00			CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT
1dcq A 685 881 1.4¢-21 -0.07 0.65	881 1.4e-21 -0.07	1.4e-21 -0.07	-0.07		0.65			PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC- BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
lib A 697 866 1.7c-30 0.22 1.00	866 1.7e-30 0.22	1.7e-30 0.22	0.22		00:1			CYCLIN-DEPENDENT KINASE 6 INFIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18- INKAC(INKO), CELL CYCLE INHIBITOR, P18-INKAC(INKO), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR.
liib A 748 894 6.80-32 0.52 1.00	894 6.8c-32 0.52	6.86-32 0.52	0.52		00'1			CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18- DIK4C(INK6), CELL CYCLE INHIBITOR, P18-INK4C(INK6), MKYRIN REPEAT, 2 CDK 446 INHIBITOR
lika D 640 812 1.7c-31 0.21 0.31	812 1.7e-31 0.21	1.7e-31 0.21	0.21		0.31			NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-	TRANSCRIPTION FACTOR P65, P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX

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PDB annotation		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR, IKBAFKR COMPLEX		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX
Coumpound	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D SUBUNIT: CHAIN: C: 1-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; 1-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	F;		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	Ę.		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPEA; CHAIN: E,	F.		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;
SEQFOL D score																																
PMF		1.00			90.			1.00				9.				0.88					1.00					1.00					1.00	
Verify score		0.10			0.37			0.52				0.37				0.15					0.43					0.42					0.50	
Psi Blast		3e-34			3.4e-38			3e-41				3e-38				1.7e-31					7.5e-34					8.5e-38					3e-35	
END AA		912			882			947				983				812					606					882					982	
STAR T AA		693			722			747				176				640					693					721					776	
CHAI N ID		Q			Ω			Ω				Δ				ST)					ш					Э					m	
aga ag		likn			lika			likn]	E				Jul.					TI					THI.					IIII	
SEQ B B SEQ		1503			1503			1503			1	1503				1503					1503					1503					1503	

PDB annotation	(TRANSCRIPTION REGULATION/ANK REPEAT), ANK YRIN 2 REPEAT HELIX	TRANSFERASE PARP-CF, POLY (ADP-RIBOSE) TRANSFERASE, POLY TRANSFERASE, GLYCOSYLTRANSFERASE, NAD(+) 2 ADP-RIBOSYLTRANSFERASE	TRANSFERASE PARP-CF,	POLY(ADP-RIBOSE) TRANSFERASE, BOLY OF TRANSFERASE,	GLYCOSYLTRANSFERASE, NAD(+)	2 ADP-RIBOSYLTRANSFERASE	COMPLEX (TRANSCRIPTION REGIT ATTON/DNA) GARPAL PHA:	GABPBETAI: COMPLEX	TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	FRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	KEGULATION/DNA) GABPALPHA;	GABLES AT COMPLEX	REGIT ATTON/DNA DNA-BINDING	2 NITCHEAD DECITED ETC DOMAIN	ANKYRIN REPEATS.	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX	IKANSCRIPTION
Coumpound	1-KAPPA-B-ALPHA; CHAIN: E, (F; F;	POLY (ADP-RIBOSE) POLYMERASE; CHAIN: NULL; P P P P P P P P P P P P P P P P P P	POLY (ADP-RIBOSE) 1	POLYMERASE; CHAIN: NULL; F			GA BINDING PROTEIN ALPHA; CHAIN: A: GA BINDING	K.B.		144	ei.	~!	\dashv	ALPHA;	CHAIN: A; GA BINDING				***		GA BINDING PROTEIN ALPHA;	_	HAIN: B;	DNA; CHAIN: D, E;
SEQFOL D score																								
PMF		0.52	0.16				1.00			_				1.00							98.0			
Verify score		0.01	-0.24				0.46							0.27							0.15			
Psi Blast		le-35	1.7e-08				3.4e-35							0.8e-39							1.7e-36			
END		1128	1127				296							373							357			
STAR T AA		958	994				128						,	22							215			
CHAI N ID							е						,	n							В			
EDB TD		1a26	1a26				lawc							Tawc							Iawc			
SEQ NO.		1504	1504				1504						1027	1204							1504			

PDB annotation	REGILATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANK YRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION BEGULATIONION) AGBALDEHA; GABBETAL; COMPLEX (TRANSCRIPTION BEGULATIONIONA), DIA-BINDING, BEGULATIONIONA), DIA-BINDING, A NUCLEAR PROTEIN, ETS DOMAIN, ANKTRIN REPEAT, ST TRANSCRIPTION 3 PACTOR	COMPLEX (TRANSCRIPTION REGILATION/DN) AGBALDHA; GABBETAH; COMPLEX (TRANSCRIPTION REGILATION/DNA), DNA-BINDING, REGILATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEN, ETS DOMAIN, ANKTRIN REPEAT, THE	COMPLEX (TRANSCRIPTION REGILATIONIDAS), OBSALPHA; GABBETAL; COMPLEX (TRANSCRIPTION BEGILA, ATIONIDA), DIA, BINDING, REGILA, ATIONIDAN, DIA, BINDING, ANKYRI REPEAT, TRANSCRIPTION 3 PACTOR	COMPLEX (TRANSCRIPTION REGULATIONIDAY) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATIONIDAY), DNA-BINDING, 2 NUCLEAR ROTEIN, ETS DOMAIN.
Commpound		GA BINDING PROTEIN ALPHA; GARIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIR: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	GA BINDIAG PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;
SEQFOL D score					
PMF	,	00:1	1:00	1.00	0.95
Verify score		0.62	0.75	0.69	0.17
Psi Blast		3e-43	1.5e-39	1.2e-33	1.2e-37
END		164	9/1	482	578
STAR T AA		25	26	335	402
CHAI N ID		æ	en.	ga .	В
804 E		lawc	Iawc	lawc	lawc
SEQ NO:		1504	1504	1504	1504

				_		_		_	_		_	_	_		_	_	_		_	_	_	_	_		_	_	_
PDB annotation	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GARPRETAL: COMPLEX	(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN.	ANKYRIN REPEATS, TRANSCRIPTION 3 PACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETAL; COMPLEX	REGULATION/ONA), DNA-BINDING	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA:	GABPBETAI; COMPLEX	(IKANSCRIPTION	KEGULA HON/DNA), DNA-BINDING,	ANK VRIN REPEATS	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX	(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 PACTOR
Coumpound		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1: CHAIN: B:	DNA; CHAIN: D, E;			GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BEI'A I; CHAIN: B;	Diet, carmin p, p,				GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA I; CHAIN: B;	DNA; CHAIN: D, E;				GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;				
SEQFOL D score													105.28														
PMF		1.00				1.00								_						1.00			_				
Verify score		0.04				67.0														0.47							
Psi Blast		3.4e-33				4.5e-47							4.5e-47							8.5e-39							
END		611				644							644							940							
STAR T AA		437				491							491							496							
CHAI		В				B							м							В							
EDB EDB		lawc				lawe							lawc							lawc							_
SEQ No.		1504				1504							1504			_				1504	_						_

nd PDB annotation	IN A ALPMA, COORNEEX PRENCERPON ING REGULATION/DOM, GARBALPHA; HANE B; CRABEERT, COMPLEX (TRANSCREPTON, DAW, BENDING, 2 NUCLEAR PROTEIN, ETS DOMAN, TRANSCREPTION 3 FACTOR	Ŕ	MA ALPHA, COMELEX (TRANSCRIPTION) THO ARRANGE TO COMELEX (TRANSCRIPTION) TRANSCRIPTION AND A CARPERALITY, COMPLEX (TRANSCRIPTION A) TO NUCLEAR PROTEIN TRANSCRIPTION 3 FACTOR TRANSCRIPTION 3 FACTOR	IN A ALPM, COMBLEX TREASCRIPTORY ING REGULATION/DASJ, COMPLEX GRANBER, COMPLEX GRANBERGETON Z NUCLEAR PROTEIN TRANSCRIPTON	İ
L Coumpound	GA BINDING PROTEIN ALPHA; CHAIN, A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHANIN, GE BINDING PROTEIN BETA 1; CHAIRE B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHANIN, GO BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: 4, GA BINDING PROTEIN BETA 1; GHAIN: B; DNA; CHAIN: D, E;	EPHA4 RECEPTOR TYROSINE
SEQFOL D score					
PMF	1.00	1.00	0.1	1.00	1.00
Verify	0.64	0.49	0.28	00.0-	1.27
Psi Blast	3e-42	3.4c-38	1.2e-35	1.4e-40	9e-07
END	784		817	296	933
STAR T AA	545	099	683	&	877
CHAI	m m	ш	ш	Д	4
PDB ED	lawc	lawc	lawc	lawc	160x
SEQ NO EI	1504	1504	1504	1504	1504

PDB annotation	INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2 DIMERIZATION DOMAIN,	TRANSPERASE SIGNAL TRANSDUCTION SAM DOWAIN, EPH RECEPTOR, SIGNAL TRANSPIPETION OF IGOMER	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTH	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTTF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,
Coumpound		EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;	EPHB2; CHAIN: A, B, C, D, E, F, G, H;	EPHB2; CHAIN: A, B, C, D, E, F, G, H;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;
SEQFOL D score											
PMF		1.00	0.99	66'0	1.00	1.00	1.00	0.98	1.00	1.00	1.00
Verify		80'1	0.82	0.72	0,43	0.67	29'0	0.13	0.14	0.82	60.0
Psi Blast		3.4e-06	0.00014	4.5e-10	4.5e-36	3e-39	le-28	3e-34	7.5e-39	1.5e-42	1.5e-41
END AA		941	935	933	317	164	483	185	614	643	701
STAR T AA		24.8	875	24.8	179	24	332	402	433	492	525
CHAI		<	4	¥							
PDB		1b0x	164f	1b4f	1bd8	8P91	1bd8	1bd8	16d8	8pqI	8pq1
SEQ NO:		1504	1504	1504	1504	1504	1504	1504	1504	1504	1504

					I .			,		
PDB annotation	ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIA-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHABETA, COMPLEX (INHIBITOR PROTEINKINASE)	COMPLEX (INHIBITOR PROTEINKINASSI) PRHIBITOR PROTEIN, CYCLIA-DEPENDENT KINASE, CHI. CYCLE 2 CONTROJ, ALPHABETA, CONFLEX (INHIBITOR PROTEINKINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT			
Coumpound		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PIGINK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9TNK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; PI9INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL D score										
PMF		1.00	0.94	1.00	00:1	66.0	0.53	1.00	10:0	1.00
Verify		0.31	0.09	0.50	0.51	0.47	-0.32	0.45	-0.31	0.60
Psi Blast		6e-41	4.5e-39	3e-41	16-28	1.4e-28	1.2e-37	1.5e-35	1.26-31	1.5e-39
END AA		191	266	784	800	818	299	317	459	164
STAR T AA		594	62	44	099	683	88	179	248	56
CHAI N ID								en.	æ	В
PDB ID		8pqI	8pqI	1bd8	1bd8	Ibd8	SpqI	1blx	1blx	1blx
SEQ ID NO:		1504	1504	1504	1504	1504	1504	1504	1504	1504

PDB ID	CHAI N ID	STAR T AA	AA AA	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
									KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHBITOR PROTEN/KINASE)
	ш	332	483	4.5e-30	0.49	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19NK 4D; CHAIN:	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR
								, B	PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL,
									ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
	B	435	618	1.5e-41	0.34	66.0		CYCLIN-DEPENDENT KINASE	COMPLEX (INHIBITOR
								6; CHAIN: A; P19INK4D; CHAIN: B;	PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT
									KINASE, CELL CYCLE 2 CONTROL,
									(INHIBITOR PROTEIN/KINASE)
	В	494	643	7.5e-42	0.72	1.00		CYCLIN-DEPENDENT KINASE	COMPLEX (INHIBITOR
								6; CHAIN: A; P19INK4D; CHAIN:	PROTEIN/KINASE) INHIBITOR
								r)	KINASE, CELL CYCLE 2 CONTROL.
									ALPHA/BETA, COMPLEX
									(INHIBITOR PROTEIN/KINASE)
	В	294	1771	4.5e-45	0.17	1.00		CYCLIN-DEPENDENT KINASE	COMPLEX (INHIBITOR
								6; CHAIN: A; P19INK4D; CHAIN:	PROTEIN/KINASE) INHIBITOR
								Ď.	KINASE CELL CYCLE 2 CONTROL
									ALPHA/BETA, COMPLEX
									(INHIBITOR PROTEIN/KINASE)
	В	648	784	9e-40	0.59	1.00		CYCLIN-DEPENDENT KINASE	COMPLEX (INHIBITOR
								6; CHAIN: A; FISHNALD; CHAIN: B:	PROTEIN/ALIVASE) INSIBILIOR PROTEIN, CYCLIN-DEPENDENT
									KINASE, CELL CYCLE 2 CONTROL,
									ALPHA/BETA, COMPLEX
	ļ,	033	000	1	120	00		TO 1 2 IN THE COLUMN TWO IS NOT THE COLUMN T	(INHIBITOR PROTEIN/KINASE)
YIOI	q	000	٦	8.26-28	0.54	1.00		CYCLIN-DEPENDENT KINASE	COMPLEX (INHIBITOR

PDB annotation	PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (NEHBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEINER PROTEINGNASE) PRIBITOR PROTEIN, CYCLIA-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHADETA, CONVELEX (INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P1 BINK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR PIS- INK4C; CELL CYCLE INHIBITOR, PI BINK4C; TIMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-
Coumpound	6; CHAIN: A; PI9INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INKAD; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE
SEQFOL D score								
PMF	1	0.99	0.92	1.00	1.00	1.00	1.00	1.00
Verify		0:30	0.28	0.85	0.64	0.57	0.63	0.27
Psi Blast		1.4e-28	1.7e-36	1.2e-35	1.4e-32	5.1e-33	6e-35	3e-35
END		818	334	176	040	802	617	164
STAR T AA		683	182	28	496	663	485	49
CHAI N ID		æ	¥.	<	Ą	A	٧	A
PDB 1D		1blx	1bu9	1bu9	lbu9	lbu9	1d9s	1d9s
SEQ ID NO:		1504	1504	1504	1504	1504	1504	1504

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PDB annotation	HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INTESTION, F18-INNAC(INNS), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR	CELL CYCLE INHIBITOR P18-	NK4C(INK6); CELL CYCLE	ANIXADELIOR, PIS-INK4C(INK6),	ANKIKIN KEFEAL, Z CLA 4/6 INHIBITOR	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6 INITIDITION	CELL CYCLE INHIBITIOR P18-	INK4C/INK6): CELL, CYCLE	INHIBITOR, P18-INK4C(INK6).	ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR	TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65;
Соптроинд	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;		CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;			CYCLIN-DEPENDENT KINASE	6 INHIBITOR: CHAIN: A. B.	6 5			NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;
SEQFOL D score										_																	
PMF		1.00	0.45	1.00			1.00				1.00				100	3				0.00			000	0.30			1.00
Verify		0.32	0.17	0.40			0.84				89.0				0.47					-0.18			000	-0.38			0.36
Psi Blast		7.5e-38	6e-37	8.5e-36			1.2e-35				1.4e-32				1.7e-32					1.2e-35				1.7e-33			1.5e-48
END	İ	643	770	333			176				640				801	;				366				403			240
STAR		517	585	182		-	28				496				663	3				156			0.00	210			28
CHAI N ID		<	A	A			\ \				A				4	:				۵			1				D
E GI		1d9s	1d9s	lihb			lihb				lihb	_			lihb	1				liki				E I			likn
SEQ NO.		1504	1504	1504			1504				1504				1504					1504			,00.	1504			1504

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PDB annotation	PSOD; TRANSCRIPTION FACTOR, IKBANFKB COMPLEX	TRANSCRIPTION FACTOR P65. P50D: TRANSCRIPTION FACTOR, IKBNFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBAFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBNPKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBNFKB COMPLEX	TRANSCRIPTION FACTOR P65; PSOD; TRANSCRIPTION FACTOR, IKBAPFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBNFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBNFKB COMPLEX	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN,
Соипроил	CHAIN: A, NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NP-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D:	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN; A; NF-KAPPA-B P50D SUBUNIT; CHAIN; C; 1-KAPPA- B-ALPHA; CHAIN; D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; 1-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B PS0D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL
SEQFOL D score										
PMF		0.30	90.0	0.55	0.25	0.92	0.80	0.12	86.0	1.00
Verify		-0.26	-0.26	-0.05	-0.36	0.20	-0.05	-0.19	0.09	0.57
Psi Blast		1.4e-30	5.1e-34	09-99	1.7e-36	1.7e-36	8.5e-40	4.5e-40	3e-35	6e-30
END		562	715	77.5	748	817	296	396	317	482
STAR		399	525	528	558	672	06	91	213	365
CHAI N ID		Д	Q	Д	Q	Q	О	О		
PDB		likn	nik	likn	nki nk	likn	likn	lika	lmyo	Imyo
SEQ UD NO:		1504	1504	1504	1504	1504	1504	1504	1504	1504

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PDB annotation	ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN,	ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN,	ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANN TRIN 2 REPEAT FIELD	COMPLEX (TRANSCRIPTION PECANIC PEPEA TO COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX
Coumpound		MYOTROPHIN; CHAIN: NULL		MYOTROPHIN; CHAIN; NULL	MYOTROPHIN; CHAIN: NULL		MYOTROPHIN; CHAIN: NULL	NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	ů.		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	i.,		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	i.		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	Ţ,	O t variable to the cutter of the	NF-KAPPA-B POS, CHAIN; A, C;	I-KAPPA-B-ALPHA: CHAIN: E.	F.	
SEQFOL D score																															
PMF		1.00		1.00	1.00		98.0	0.58					0.93					0.36				,	96.0				19.0	1+10			
Verify score		0.51		0.03	99.0		0.57	-0.11					-0.17					-0.34					-0.01				90.0	0.00			
Psi Blast		3e-39		1.5e-38	7.5e-39		6.8e-25	6.8e-36					1.5e-40					1.2e-44					5.1e-33				1 5- 50	1.35-30			
END AA		644		165	794		662	998					424					458					403				600	770			
STAR T AA		528		19	681		684	154					154					208				000	506				276	202			
CHAI N ID								ш					ш					щ					21				E	q			
PDB TD		lmyo		lmyo	lmyo		lmyo	IJul					Jufi					Juli					Ē				I m 62				
SEQ NO.		1504		1504	1504		1504	1504					1504					1504				700	1504				1504	5			

PDB annotation	COMPLEX (TRANSCRIPTION REGANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANK YRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REGGANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANK YRN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REGANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REGIANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANK YRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REGVANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT),
Coumpound	NF-KAPPA-B P65; CHAIN: A, C, NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65, CHAIN: A, C, NF-KAPPA-B P50; CHAIN: B, D, FKAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P60; CIAMN: B, D; I-KAPPA-B-ALPHA; CHAIN: B, F;	NF-KAPPA-B P65, CHAIN: A, C, NF-KAPPA-B P50; CHAIN: B, D, I-KAPPA-B-ALPHA; CHAIN: E, F;	NP-KAPPA-B P65, CHAIN: A, C; NP-KAPPA-B P50; CHAIN: B, D; F: F;	NP-KAPPA-B P65; CHAIN: A, C; NP-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;
SEQFOL D score							
PMF	0.95	00.1	66.0	00.1	67:0	00:1	86.0
Verify	0.08	0.35	0.34	-0.06	-0.13	0.22	0.12
Psi Blast	3e-45	5.1e-37	1.70-32	6e-57	1.36-54	1.7c-36	6.8e-40
END	643	829	682	111	307	817	296
STAR	429	463	490	528	61	672	88
CHAI N ID	ш	ш	ш	ш	ш	ш	ш
PDB	lufi	Jul	Infi	lnfi	Infi	JII.	lnfi
SEQ NO:	1504	1504	1504	1504	1504	1504	1504

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PDB annotation	ANKYRIN 2 REPEAT HELIX	TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION, EPH RECEPTORS, TYROSINE 2 PHOSPHORYLATION, SIGNAL TO ANNOMICTION TYPOGOME	PROTEIN 3 KINASE	TYROSINE-PROTEIN KINASE NMR, RECEPTOR OF IGOMERIZATION	EPH RECEPTORS, TYROSINE 2	PHOSPHORYLATION, SIGNAL	TRANSDUCTION, TYROSINE- PROTEIN 3 KINASE	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE	COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)	P53BP2; ANKYRIN REPEATS, SH3,	P53, TUMOR SUPPRESSOR,	MULTIGENE 2 FAMILY, NUCLEAR	PROTEIN, PHOSPHORYLATION,	DISEASE MUTATION, 3	POLYMORPHISM, COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)	P53BP2; ANKYRIN REPEATS, SH3,	P53, TUMOR SUPPRESSOR,	MULTIGENE 2 FAMILY, NUCLEAR	PROTEIN, PHOSPHORYLATION,	DISEASE MUTATION, 3	POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)
Coumpound		EPIRIN TYPE-B RECEPTOR 2; CHAIN: NULL;		EPHRIN TYPE-B RECEPTOR 2;	1			REGULATORY PROTEIN SWI6;	CHAIN: A, B;	P53: CHAIN: A: 53BP2: CHAIN:	B								P53; CHAIN: A; 53BP2; CHAIN:	B						
SEQFOL D seore																										
PMF		0.84		0.59				0.18		0.84									1.00							
Verify		0.65		0.78				-0.22		-0.13									-0.03							
Psi Blast		0.00034		1.5e-09				6e-37		6e-30									4.5e-40							
END		935		933				784		569									722							
STAR T AA		875		877				527		366									528							
CHAI N ID								A		В									В							
eg e		lsgg		1888				1sw6		1vcs									lycs							
SEQ NO.		1504		1504				1504		1504									1504							

PDB annotation	ONCOGENEZ (ANT) ONCOGENEZ (ANT) ONCOGENEZ (ANT) ONCOGENEZ (ANT REPEATS, SIE3, PEST, TUMOR SUPPLESOR) PEST (TUMOR SUPPLESOR) PROTEIN PROSPERORYL/INCLEAR PROTEIN PROSPERORYL/INCLEAR PROTEIN PROSPERORYL/INCLEAR PROTEIN PROSPERORYL/INCLEAR ONCOGENIZ/ANG/PERSA (CAPPLESORY) ONCOGENIZ/ANG/PERSA (CAPPLESORY)	HYDROLASE TETRATRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELLX, X-RAY STRUCTURE	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION		SIGNALLING COMPLEX RACI; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTH	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL
Coumpound	P5; CHAIN: A; 53BP2; CHAIN: B;	SERINETHREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	TRANSCRIPTION FACTOR PML; CHAIN: NULL;	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	RAS-REI ATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A: NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN:
SEQFOL D score							
PMF	0.76	0.05	0.13	0.82	-0.03	0.31	-0.02
Verify score	0.01	-0.10	-0.76	-0.25	0.02	0.05	0.00
Psi Blast	7.5e-39	1.7e-29	3e-14	6e-14	3,4e-14	6.8e-22	1.5e-11
END	254	190	262	262	191	161	110
STAR T AA	59	39	218	221	40	39	24
CHAI N ID	m				В	v.	A
FDB ID	lyes	la17	Ibor	1chc	1e96	lefr	Ielw
SEQ El Si ON	1504	1507	1507	1507	1507	1507	1507

PDB annotation	REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING FINGER (C3HC4)	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING RECOMBINATION, ANTIBODY, RECOMBINATION, ANTIBODY, MAD, RIVO FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC BINUCLEAR CLUSTER, ZINC	COMPLEX (CMAUNGGLOBULIN/AUTOANTIGE N) COMPLEX (RMAUNGGLOBULIN/AUTOANTIGE N), RHEUMATOID FACTOR 2 AUTO- ANTIBODY COMPLEX	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	NSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING,
Coumpound	C, D;	TPRI-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI; CHAIN: A:	AN: NULL;	IGG4 REA; CHAIN; A; RF-AN IGM/LAMBDA; CHAIN; H, L;	HEMOLIN; CHAIN: A, B;	HEMOLIN; CHAIN: A, B;	HEMOLIN; CHAIN: A, B;	HEMOLIN; CHAIN: A, B;
SEQFOL D score									124.44
PMF		0.24	0.37	0.84	0.64	0.39	0.49	96'0	
Verify score		0.13	-0.20	0.13	-0.07	0.18	0.34	0.29	
Psi Blast		1.46-21	4.5e-13	96-17	8.5e-18	5.1c-43	1.5e-43	1.7e-50	1.7e-50
END		153	262	302	531	829	721	812	813
STAR T AA		39	221	210	352	292	350	644	450
CHAI N ID		V	¥		1	٧	٧	¥	V
PDB		lelw	1g25	Irmd	Ipadq	1bih	16ih	1bih	1bih
SEQ No.		1507	1507	1507	1508	1508	1508	1508	1508

PDB annotation	HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING,	HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT	IMMUNITY, LPS-BINDING,	HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT	IMMUNITY, LPS-BINDING,	HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT	IMMUNITY, LPS-BINDING,	HOMOPHILIC ADHESION	T-CELL SURFACE GLYCOPROTEIN	IMMUNOGLOBULIN FOLD,	TRANSMEMBRANE,	GLYCOPROTEIN, T-CELL, 2 MHC,	LIPOPROTEIN, T-CELL SURFACE	GLYCOPROTEIN	CELL ADHESION NEURAL CELL	ADribaiOn	CELL ADHESION NEURAL CELL		CELL ADHESION NEURAL CELL ADHESION	CELL ADHESTON NET BAT. CELL.	ADHESION	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL	ADHESION	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL
Coumpound		HEMOLIN; CHAIN: A, B;		HEMOLIN; CHAIN: A, B;			HEMOLIN; CHAIN: A, B;			HEMOLIN; CHAIN: A, B;			T-CELL SURFACE	GLYCOPROTEIN CD4; CHAIN:	NULL;				AXONIN-1; CHAIN: A;		AXONIN-1; CHAIN: A;		AXONIN-1; CHAIN: A;	AXONIN-1: CHAIN: A:		AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;		AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;
SEQFOL D score																														
PMF		-0.07		0.36			0.49			0.21			0.42						0.53		0.41		0.62	-0.01		0.84	0.70		80.0-	-0.02
Verify		0.00		0.15			90.0			0.18			0.42						-0.05		0.07		0.15	0.08		0.26	0.24		0.05	0.07
Psi Blast		5.1e-37		6.8e-40			4.5e-37			3.4e-46			1.5e-15						8.5e-49		1.5e-49		5.1e-65	le-44		3.4e-55	5.1e-49		6.8e-37	7.5e-39
END . AA		335		1073			447			1184			723						535	1	628	, 00	17/	347		813	268		448	448
STAR		4		726			74			816			557						178		292	9,0	348	3		449	536		Z	74
CHAI N ID		¥		A			٧			¥									٧	-	<		<	A		۷	~		<	¥
EDB OI		1bih		1bih			1bih			Ibih			lcdy						1cs6		lcs6		Icse	1cs6		lcs6	1cs6		1036	lcs6
SEQ NO:		1508		1508			1508			1508			1508						1508	0000	1508	000	8001	1508		1508	1508		1508	1508

	CHAI N ID	STAR	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
								The state of the s	TOTOLINA
									ADHESION
	A	829	1185	8.5e-48	0.04	0.24		AXONIN-I; CHAIN: A;	CELL ADFESION NEURAL CELL ADFESION
	C	6001	1184	1.7e-38	0.13	-0.01		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH
								FACTOR 2; CHAIN: A, B;	FACTOR RECEPTOR FGF, FGFR,
								FIBROBLAST GROWTH	IMMUNOGLOBULIN-LIKE, SIGNAL
								FACTOR RECEPTOR 1; CHAIN:	TRANSDUCTION, 2 DIMERIZATION,
								i i	GROW HE FACTOR/GROW IN
	C	9601	1260	5.1e-21	80:0	-0.19		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH
								FACTOR 2; CHAIN: A, B;	FACTOR RECEPTOR FGF, FGFR,
								FIBROBLAST GROWTH	IMMUNOGLOBULIN-LIKE, SIGNAL
								FACTOR RECEPTOR 1; CHAIN:	TRANSDUCTION, 2 DIMERIZATION,
								C, D;	GROWTH FACTOR/GROWTH
									FACTOR RECEPTOR
	0	178	346	6.8e-21	-0.16	0.30		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH
								FACTOR 2; CHAIN: A, B;	FACTOR RECEPTOR FGF, FGFR,
								FIBROBLAST GROWTH	IMMUNOGLOBULIN-LIKE, SIGNAL
								FACTOR RECEPTOR 1; CHAIN:	TRANSDUCTION, 2 DIMERIZATION,
								C, D;	GROWTH FACTOR/GROWTH
									FACTOR RECEPTOR
	o	6	146	3.4e-I7	0.23	-0.I5		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH
								FACTOR 2; CHAIN: A, B;	FACTOR RECEPTOR FGF, FGFR,
								FIBROBLAST GROWTH	IMMUNOGLOBULIN-LIKE, SIGNAL
							•	FACTOR RECEPTOR 1; CHAIN:	TRANSDUCTION, 2 DIMERIZATION,
								C, D;	GROWTH FACTOR/GROWTH
									FACTOR RECEPTOR
	ပ	361	535	5.1e-23	0.17	0.21		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH
								FACTOR 2; CHAIN: A, B;	FACTOR RECEPTOR FGF, FGFR,
								FIBROBLAST GROWTH	IMMUNOGLOBULIN-LIKE, SIGNAL
			-					FACTOR RECEPTOR 1; CHAIN:	TRANSDUCTION, 2 DIMERIZATION,
								C, D;	GROWTH FACTOR/GROWTH
	C	450	000	0 50 00	200	130		CIDD OD! 4 OF OBOTIERS	PACIUK KECEPIUK
7		420	020	0.75-20	-0.05	400		FIBROBLAST GROWIN	GROW IN FACTOR/GROW IN

PDB annotation	FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR.	GROWTH FACTOR/GROWTH PACTOR REGEPTOR FOF, EGER, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR ROSPITOR, FOR FIGH, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR REGEPTOR FOF, FGER, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FOF, FGFR, IMMUNOGLOBULN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH
Compound	FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBILAST GROWTH FACTOR S.; CHANIN. A, B; FIBROBILAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR S.; CHANIS, B.; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR S.; CHANIX.A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: G, D;	FIBROBLAST GROWTH FACTOR S.; CHANIX, A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBIAST GROWTH FACTOR 2: CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;
SEQFOL D score						
PMF		0.27	0.21	-0.05	-0.15	90.0
Verify score		-0.10	-0.42	0.07	0.05	0.23
Psi Blast		5.1e-24	8.5e-36	1.7e-24	1.7e-37	5.1e-34
END		260	812	968	966	1184
STAR T AA		19	642 .	737	813	1000
CHAI N ID		υ	υ	v	O	Д
PDB		lcvs	icvs	lcvs	Icvs	Icvs
SEQ.		1508	1508	1508	1508	1508

PDB annotation	PTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF. FGFR.	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACIOR RECEPTOR	TOK/GKOWIH	FACTOR RECEPTOR FOF, FOFR,	TRANSDUCTION, 2 DIMERIZATION.	GROWTH FACTOR/GROWTH	PTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	SPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	PTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	PTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,
PD	FACTOR RECEPTOR	GROWTH FAC	IMMUNOGLO	TRANSDUCTION	GROWTHFAC	Chourt RECEPTOR	GKOW IH FAC	IMMI INOGLO	TRANSDICT	GROWTH FAC	FACTOR RECEPTOR	GROWTH FAC	FACTOR RECE	IMMUNOGLO	TRANSDUCTION	GROWTH FAC	FACTOR RECEPTOR	GROWTH FAC	FACTOR RECE	IMMUNOGEO	TRANSDUCTION	GROWTH FAC	FACTOR RECEPTOR	GROWTHFAC	FACTOR RECE	IMMUNOGLO!	TRANSDUCTI	GROWTH FAC	FACTOR RECEPTOR	GROWTH FAC	FACTOR RECE
Coumpound		FIBROBLAST GROWTH FACTOR 2: CHAIN: A. B:	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;	THE PART AND THE PARTY	FISKUBLASI GROWIN	FACTOR 2; CHAIN: A, B;	PACTOR RECEPTOR 1: CHAIN:	C, D;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	Ç, Ç;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;
SEQFOL D score																															
PMF		0.82				100	0.0					-0.05						0.25						0.71						0.30	
Verify score		-0.19				21.0	0.15					0.19						61.0						-0.02						0.13	
Psi Blast		1.2e-21				14.00	1./6-33					6.8e-19						8.5e-25						3.4e-35						1.2e-22	
END		346				277	/#					146						535						628			_			260	
STAR		178				100	1//7					2						361						450						61	
CHAI N ID		Д					٦.					۵						Ω						Д						Ω	
PDB ED		Icvs					SAST					Icvs						Icvs						lcvs						lcvs	
SEQ NO.		1508				1500	oner					1508						1508						1508						1508	

		_										_						_						_					
PDB annotation	TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	ON OWNERS TO COLOUR ON OWNERS AND INC.	GROWIN FACTON/GROWIN FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	VIRUS/VIRAL PROTEIN, RECEPTOR	CD155, PVR, HUMAN POLIOVIRUS,	ELECTRON MICROSCOPY, 2	POLIOVIRUS-RECEPTOR COMPLEX,	VIRUS/VIRAL PROTEIN, RECEPTOR	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS,
Coumpound	FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR NECEFIOR I; CHAIN.		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;		POLIOVIRUS RECEPTOR;	CHAIN: R; VPI; CHAIN: 1; VP2;	CHAIN: 2; VP3; CHAIN: 3; VP4;	CHAIN: 4;		POLIOVIRUS RECEPTOR; CHAIN: R; VPI; CHAIN: 1; VP2;
SEQFOL D score																													
PMF		0.00					90.0					-0.11						0.00						0.03					0.16
Verify		-0.31					0.11					0.04						0.20						-0.35					-0.09
Psi Blast		1.2e-36					1.7e-25					3.4e-34						3.4e-23						6e-22					1.3e-23
END AA		812					968					966						1082						810					688
STAR T AA		642					737				-	813						911						602					641
CHAI N ID		Q					D					Ω						۵						ద					~
PDB CI		lcvs					Icvs					lcvs						lcvs						1dgi					Idgi
SEQ No.		1508					1508			_		1508						1508						1508					1508

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PDB annotation	IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR REGETOR FORZ; FOFRZ; IMMUNOGLOBULIN (GIJJKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN (G-LIKE DOMAINS, B-I'REFOLI, FOLD	GROWTH FACTOR/GROWTH FACTOR REGEPTOR FRIZE, FGFR2, IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN (G-LIKE DOMAINS, B-TREFOIL, FOLD.	GROWTH FACTOR/GROWTH FACTOR REGEPTOR FGFF2, FGFR2, IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOII, FOLD	GROWTH FACTOR/GROWTH FACTOR REGETOR RGF2, FGFR2, IMMUNOGI, OBULIN (GGLIXE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHN IG-LIKE DOMAINS, B-TREFOLL, FOLL DOMAINS, B-TREF	GROWTH FACTOR/GROWTH FACTOR REGETOR FIGTS, FGFR2, RAMUNOGLOBULIN (GGLIAR) DOMAINS BELONGING TO THE I- SETT SCHORGROUP THIN IGELIKE DOMAINS REFERENT FOIL DOMAINS REPRESENT FOIL
Coumpound	FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBI AST GROWTH FACTOR 2; CHANIA, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: B, F, G, H;	FIEROBLAST GROWTH FACTOR S. CHANIA, A. B., C. D., FIEROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: B. F. G. H;	FIBROBLAST GROWTH FACTOR 2, CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2, CHAIN: E, F, G, H;	FIBROBLAST GRÖWTH FACTOR 2, CHAIN: A, B, C, D, FIBROBLAST GROWTH FACTOR RECEPTOR 2, CHAIN: E, F, G, H;	FIEROBLAST GROWTH FACTOR S. CHANIA, B, C, D, FIEROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: B, F, G, H;
SEQFOL D score						
PMF		0.04	0.07	-0.11	0.01	0.43
Verify		0.10	-0.05	0.06	0.10	0.02
Psi Blast		5.1e-22	1e-33	1.7e-31	5.1c-35	8.5e-21
END		535	628	966	1188	350
STAR T AA		361	454	825	1009	178
CHAI N ID		ш	ш	Þì	Đ	5
PDB DI		lev2	lev2	lev2	lev2	lev2
S B S		1508	1508	1508	1508	1508

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PDB annotation	GROWTH PACTORGROWTH PACTOR RECETOR FGP2, IMMUNOGLOBULIN (IG)LIKE DOMANINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMANINS, B-TREFOLL FOLL	GROWTH PACTORGROWTH PACTOR RECEPTOR FGPS, FGPRS, IMMUNOGLOBULIN (19)LIKE DOMAINS BELONGING TO THE I. SET 2 SUBGROUP WITHIN IG-LIKE DOMANNS, B-TREPOIL, POLID	GROWTH FACTOR/GROWTH PACTOR REGETOR FGPR2, IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I. SET 2 SUBGROUP WITHIN (IG-LIKE DOMANNS, B-TREPOLL FOLD	GROWTH PACTOR/GROWTH PACTOR REGEPTOR FGPR2, IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE 1- SET 2 SUBGROUP WITHIN (G-LIKE DOMANS, B-TREPOLL FOLD	GROWTH FACTOR/GROWTH PACTOR REGEPTOR FORZ; PACTOR REGEPTOR MAUTNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS. B-TREFOLL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE
Coumpound	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2, CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2, CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2, CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2, CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR PROFESSION 2; CHAIN:
SEQFOL D score						
PMF	-0.05	0.18	69.0	90.0	0.53	0.17
Verify	0.01	0.13	0.41	-0.02	0.23	0.12
Psi Blast	8.5e-18	1.2e-32	6.8e-24	6.8e-34	1.7e-23	1.2e-21
END	152	451	538	628	724	264
STAR T AA	-	27.1	361	454	549	19
CHAI N ID	Đ	0	9	0	5	9
EDB ID	lev2	lev2	lev2	lev2	lev2	lev2
SEQ NO:	1508	1508	1508	1508	1508	1508

PDB annotation	SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD		,	GROWTH FACTOR/GROWTH D; PACTOR REGETOR FOR FGIRZ, IMMUNOGLOBULIN (GI)LIKE DOMANINS BELONGING TO THE I. SET 2 SUBGROUP WITHIN IG-LIKE DOMANINS, B-TREPOIL, FOLL	GROWTH EACTOR/GROWTH D; PACTOR REGEPTOR FORP; GFR2; IMMUNOGLOBULIN (G)LIKE DOMANNS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMANNS, B-TREPOIL, FOLL	GROWTH FACTOR/GROWTH D; PACTOR KEGETVOR FORP; FORR2, IMMUNOGLOBULIN (G),LIKE INMENOGLOBULIN (G),LIKE DOMAINS BELONGING TO THE I. SET 28 USBGROUP WITHIN IG-LIKE DOMAINS. B-TREFOLL FOLL	GROWTH FACTOR/GROWTH
Coumpound	E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D, FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D, FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2, CHAIN: A, B, C, D, FIBROBLAST GROWTH FACTOR RECEPTOR 2, CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH
SEQFOL D score							
PMF		0.15	0.23	0.51	-0.15	-0.01	0.33
Verify		-0.35	80.0	0.18	0.04	0.02	-0.26
Psi Blast		6.8e-34	3.4e-25	1.5e-22	1.7e-33	6.8e-22	5.1e-21
END		816	006	259	1000	1087	346
STAR T AA		651	737	74	825	911	178
CHAI N ID		O	5	o	Ð	5	C
PDB ID		lev2	lev2	lev2	1ev2	lev2	levt
SEQ No.		1508	1508	1508	1508	1508	1508

				,		
PDB annotation	IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF!; FGFR!, MANUNOGLOBULN (10) LIKE DOMAINS BELONGING TO THE I. SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOLL FOLD	GROWTH FACTORGROWTH FACTOR RECEPTOR FOR!, FORR!, MANUNOGLOBULIN (1G) LIKE DOMAINS BELONGING TO THE!- SET 2 SURGROUP WITHIN IG-LIKE DOMAINS, B-TREFOLL FOLD DOMAINS, B-TREFOLL FOLD	GROWTH FACTORGROWTH FACTOR REGEPTOR FEBT; FGFRI; MANUNOGLOBULIN (G) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL; FOLD.	GROWTH FACTOR/GROWTH FACTOR REGEPTOR REFI; FGFR1; MAMUNOGLOBULIN (05) LIKE DOMAINS BELONGING TO THE I- SET 2 SURGROUP WITHIN IG-LIKE DOMAINS, B-TREFOLI, FOLD DOMAINS, B-TREFOLI, FOLD	GROWTH FACTORGROWTH FACTOR REGEPTOR REF!, FGFR!, MAINNOGLOBULIN (G) LIKE DOMAINS BELONGING TO THE I- SETT SCHORGROUP WITHIN IG-LIKE DOMAINS PERPERDIT POIN PLANCE PONARINS PERPERDIT POIN POINTED
Coumpound	FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIEROBLAST GROWTH FACTOR I; CHANIX, A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBIAST GROWTH FACTOR 1; CHANIX, A, B; FIBROBIAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIEROBLAST GROWTH FACTOR I; CHANIA, A, B; FIEROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR I; CHARIN, A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR I; CHAIN: FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;
SEQFOL D score						
PMF		, ,	-0.09	0.18	0.19	0.04
Verify		0.01	0.23	-0.15	-0.01	0.16
Psi Blast		8.5e-32	3.4e-19	3.4e-33	3e-16	1.2e-22
END AA		447	146	928	703	260
STAR		271	2	450	552	19
CHAI N ID		o	ပ	o	o	v
EDB TO		levt	levt	levt	levt	levt
SEQ NO:		1508	1508	1508	1508	1508

РDВ аппоtation	GROWTH FACTORGROWITH FACTOR RECEPTOR FGF1; FGFR1; MAMUNOGLOBULIN ((G) LIKE DOMANINS BELONGING TO THE 1- SET 2 SUBGROUP WITHIN IG-LIKE DOMANINS, B-TREFOLL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; MARDNOGLOBULIN (1G) LIKE DOMANINS BELONGRING TO THE; SET 2 SUBGROUP WITHIN 16-LIKE DOMANINS, B-TREFOLL FOLD.	IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM PC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM FC-EPSILON RI- ALPHA: IMMUNOGLOBULIN FOLD,
Coumpound	FIBROBIAST GROWTH FACTOR I; CHAIN: A, B; FIBROBIAST GROWTH FACTOR RECEPTOR I; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR I: CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR I; CHAIN: C, D;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	HIGH APFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON			
SEQFOL D score								
PMF	0.11	-0.03	90'0	0.48	0.92	0.63	0.17	0.12
Verify score	-0.32	0.05	0.14	0.32	0.26	-0.01	0.05	0.04
	1.4e-35	1.2e-24	I.5e-17	3e-2I	1.5e-20	9e-I8	1.7e-21	3e-19
	812	968	538	153	539	727	795	006
STAR T AA	642	737	349	39	415	509	646	779
CHAI N ID	υ	v	<	<	V	٧	A	A
PDB ID	levt	levi	If2q	pZJ1	1 1 2q	1f2q	1129	1f2q
SEQ ID NO:	1508	1508	1508	8051	1508	1508	1508	1508

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PDB annotation	GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM HIGH AFFINITY	IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN, RECEPTOR, IGE-	BINDING 2 PROTEIN, IGE	ANTIBODI, IOE-FC	IMMUNE STSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC (EPSILON)	IGE-FC; IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN, RECEPTOR, IGE-	BINDING 2 PROTEIN, IGE	ANTIBODY, IGE-FC	IMMUNE SYSTEM FIGH AFFINITY	IGE-FC RECEPTOR, PC(EPSILON)	IGE-FC; IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN, RECEPTOR, IGE-	BINDING 2 PROTEIN, IGE	ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY	IGE-FC RECEPTOR, FC(EPSILON)	IGE-FC; IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN, RECEPTOR, IGE-	BINDING 2 PROTEIN, IGE	ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY	IGE-FC RECEPTOR, FC(EPSILON)	IGE-FC; IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN, RECEPTOR, IGE-	BINDING 2 PROTEIN, IGE	ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY	TOR-FORECEPTOR FORESTION
Coumpound	RECEPTOR CHAIN: A;	HIGH AFFINITY	RECEPTOR CHAIN: A; 1G	EPSILON CHAIN C REGION;	CHAIN: B, D;	Additional treatment	IMMUNOGLOBULIN EPSILON	RECEPTOR CHAIN: A; 1G	EPSILON CHAIN CREGION;	CHAIN: B, D;		HIGH AFFINITY	IMMUNOGLOBULIN EPSILON	KECEPTOR CHAIN: A; IG	EPSILON CHAIN CIKEGION;	CHAIN: B, D;		FIIGH AFFINITY	IMMUNOGLOBULIN EPSILON	RECEPTOR CHAIN: A; 1G	EPSILON CHAIN C REGION;	CHAIN: B, D;		HIGH AFFINITY	IMMUNOGLOBULIN EPSILON	RECEPTOR CHAIN: A; IG	EPSILON CHAIN C REGION;	CHAIN: B, D;		HIGH AFFINITY	IMMUNOGLOBULIN EPSILON
SEQFOL D score																															
PMF		0.01				00.0	-0.02					0.30						0.24						0.70						0.95	
Verify		10:0-				000	60.0					0.16						0.35						0.21						0.37	
Psi Blast		3.4e-19				24. 44	3.46-1/					6e-21						9c-20						7.5c-19						7.5e-19	
END		430				000	228					152						538						645						726	
STAR T AA		258				25.0	ę.					39						415						451						999	
CHAI N ID		¥					<					٧						٧						A						¥	
PDB		116a				195	BOLL					1f6a						1f6a					1	1f6a						If6a	
SEQ NO ID		1508				1500	9061					1508						1508						1508						1508	

PDB annotation	IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY GB-PC RECEPTOR, FOGEPSILON) GER-C IMMUNCOLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE BINDING 2 PROTEIN, IGE ANTHODY, IGE-FC	MMUNE SYSTEM HIGH AFFINITY (GB-FC RECEPTOR, FCGPSLLON) (GB-FC, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN, IGE- ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY GIB-FO REGEPTON, FOGEPSELON) GILYCOPROTEIN, RECEPTOR, IGE BINDING 2 PROTEIN, IGE ANTIRODY, IGE-FO	IMMUNE SYSTEM HIGH AFFINITY GER-C RECEPTOR, FOGEPSILON) GER-C, IMMUNGOLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32	
Coumpound	RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON IRECEPTOR CHAIN: A: 1G EPSILON CHAIN C REGION; CHAIN: B, D;	HIGH APFINITY IMMUNOGGLOBULIN EPSILON IRECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	HIGH APENUTY IMMUNOGLOBULIN EPSILON IRECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	HIGH AFFINITY IMMUNOCALOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	
SEQFOL D score							
PMF		-0.11	0.11	0.10	0.65	0.55	
Verify score		0.20	-0.14	0.27	0,11	0.38	
Psi Blast		1e-16	1.4e-20	1.5e-19	1.5e-15	1.2e-17	
END		152	795	006	666	534	The second name of
STAR T AA		ın.	946	740	821	349	
CHAI		∢	∢	4	∢	4	İ
PDB ID		1f6a	1f6a	1f6a	116a	Ifcg	
SEQ NO:		1508	1508	1508	1508	1508	

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PDB annotation	IMMUNOGLOULIN, LEUKOCYTE, CD32	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32, FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN- LIKE, RECEPTOR	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN- LIKE, RECEPTOR	CONCIEX GIVE STORYELOW PROTEINCLOMFASH COMPLEX (HV ENVELODE PROTEINCLOMFASH). HIV-1 EXTENCO ENVELODE GP120, FCELL SURRAGE BINDING FRACORDETT OF HUMAN MANINGLOGULIN 178, HUMAN GLYCOSYLTHATID PROTEIN GLYCOSYLTHATID PROTEIN	
Coumpound		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	TBLOKIN; CHAIN: A	TELOKIN; CHAIN: A	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	WINDLOPE PROTEIN GUIDO. CHAINE G. CDA: CHAIN: C. ANTIBODY 17B; CHAIN: L, H;	T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) 1HNG 3
SEQFOL D score									
PMF		0.43	0.53	0.03	0.00	0.54	0.41	0.60	90.0
Verify		0.02	-0.26	0.20	-0.28	0.29	0.03	0.17	-0.34
Psi Blast		6e-19	6.8e-17	8.5e-16	8.5e-17	3e-18	3.4e-16	1.7e-15	66-19
END		645	766	1186	447	148	796	518	703
STAR T AA		456	820	1085	347	36	949	352	557
CHAI		¥	4	₹	٧	٧	∢	7	A
PDB TD		1fcg	1fcg	1fhg	1fhg	1fnl	퍨	1gc1	Ihng
SEQ NO ID		1508	1508	1508	1508	1508	1508	1508	1508

PDB CHAI STAR END ID NID TAA AA	STAR T AA		A EN	9.4	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
lhng A 825 996 9e-15	966	966		9e-15	1	90.0	0.17		TLYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) 1HNG 3	
lith B 462 679 1.5e-20	619	619		1.5e-20		-0.02	0.18		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (MAMUNOGLOBULIN/RECEPTOR) (MAMUNOGLOBULIN/RECEPTOR) (MAMUNOGLOBULIN/POLD, TRANS/MEMBRANE, GLYCOPROTEIN, RECEPTOR, SIGNAL, COMPLEX (MAMUNOCIONI) IN/RECPTOR)
Tith B 740 996 36-20	36-20	36-20	3e-20			0.42	60.00		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMNOGLOBULINREGEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEN, RECEPTOR, 2 SIGNAL, COMPLEX
litb B 747 994 1.7e-15 C	994 1.7e-15	994 1.7e-15	1.7e-15		9	0.10	0.55		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMINOGLOBULINRECEPTOR) IMMUNOGLOBULIN FOLD, TRANSWEMBRANE, GLYCOPROTEN, RECEPTOR, 2 SIGNAL, COMPLEX, COMPLEX, COMPLEX,
1koa 1084 1185 3.4e-14 0	1185 3.4e-14	1185 3.4e-14	3.4e-14		0	0.14	0.59		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
IIII A 355 531 8.5e-16 0	531 8.5e-16	531 8.5e-16	8.5e-16		0	0.20	09'0		LAMBDA III BENCE JONES PROTEIN CLE; CHAIN: A, B	IMMUNOGLOBULIN IMMUNOGLOBULIN, BENCE JONES PROTEIN
Imco H 143 543 5.1e-17	243	243		5.1e-17				104.67	IMMUNOGLOBULIN IMMUNOGLOBULIN GI (IGGI) (MCG) WITH A HINGE DELETION 1MCO 3	
lmco H 538 884 1.5e-17	884 1.5e-17	884 1.5e-17	1.5e-17	П	1 ' 1	-0.05	0.23		IMMUNOGLOBULIN	

PDB annotation		MUSCLE PROTENT CONNECTIN, NEXTNA; CELL ADHESION, GLYCOPROTEIN, TRANNAMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN POLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN.	MURSCLE PROTEIN CONNECTIN, UNEXTMS; CELL ADHESION, GLYCOROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMAUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN	MUSCLE PROTENT CONNECTIN, NEXTM4: CELL ADHESION, GLYCOPROTEIN, TRANNAMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN POLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN	MUSCLE PROTEIN CONNECTIN, NEXTMS, CELL ADHESION, GLYCOROTEIN, RRANNSMERRANE, REPEAT, BRAIN, 2 INAUNOGLOBULIN FOLD, ALTIRENATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL
Coumpound	IMMUNOGLOBULIN GI (IGGI) (MCG) WITH A HINGE DELETION IMCO 3	TITIN, CHAIN: NULL;	TITIN, CHAIN: NULL;	TITIN; CHAIN: NULL;	TITIN; CHAIN: NULL;	P38-CL42 KIR; CHAIN: NULL;
SEQFOL D score						
PMF score		0.53	0.00	-0.12	0.04	-0.07
Verify score		0.58	-0.53	0.16	0.46	0.11
Psi Blast		1.7e-14	3.46-11	5.1e-15	1.7e-13	3.4e-10
END		1185	262	449	721	149
STAR T AA		1086	178	349	643	56
CHAI						
PDB ID		lnct	Inct	Inct	Inet	Inkr
SEQ ID NO:		1508	1508	1508	1508	1508

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PDB annotation	KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD	INHIBITORY RECEPTOR KILLER CELL NHBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, MANUNOCLOBULIN FOLD					CELL ADHESION PROTEIN VCAM- D1,2; IVCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING IVCA 15	CELL ADHESION PROTEIN VCAM-
Coumpound		PS&-CL42 KIR; CHAIN: NULL;	MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN) ITINA 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITINM 4 1TINM 58	MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN) ITMA 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITIMA 58	MUSCLE PROTEIN TITIN MODULE MS (CONNECTEN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 1TNM 58	MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN) ITUMA 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	HUMAN VASCULAR CELL ADHESION MOLECULE-1; IVCA 4 CHAIN: A, B; IVCA 5	HUMAN VASCULAR CELL
SEQFOL D score								
PMF		0.13	0.35	0.00	-0.15	0.04	0.72	0.00
Verify score		-0.01	0.63	-0.22	0:30	0.50	-0.05	-0.15
Psi Blast		1.7e-23	1.7e-14	3.4e-11	1.5e-09	1.76-13	4.5e-15	4.5e-13
END AA		995	1185	262	19	721	538	089
STAR T AA		813	1088	178	2	643	397	557
CHAI N ID							V.	A
PDB TD		lnkr	ltnm	Itnm	Itnm	Itnm	Ivca	Ivca
S a S		1508	1508	1508	1508	1508	1508	1508

FDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
		- XX	ž		score	score	D SCOLE		
								ADHESION MOLECULE-1; IVCA 4 CHAIN: A, B; IVCA 5	D1,2; 1VCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING 1VCA 15
	V	364	703	1.2e-26	0.09	0.41		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMA/UNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC TIPOPR OTFIN POI YAMORDISM
т —	<	252	882	6e-26	-0.11	0.13		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMALUNOGLOBULIN FOLD, IRANSMEMBRANB, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
	<	740	8901	6e-23	0.06	9.68		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSNEMBRANB; GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
		821	0001	1.5e-16	-0.09	0.05		INTERCELLULAR ADHESION MOLECULE-2; CHAIN: NULL;	CELL ADHESION ICAM-2; IMMUNOGLOBULIN FOLD, CELL ADHESION, GLYCOPROTEIN, 2 ATANSMEMBRANE, REPEAT, SIONAL
	∢	347	534	12e-19	0.19	-0.09		MHC CLASS INK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM PS8 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER REGEPTOR, INHIBITOR Y RECEPTOR, IMMUNOGLOBULIN
	¥	451	643	4.5e-24	0.28	0.05		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM PS8 NATURAL KULLER CELL RECEPTOR, KIR, NATURAL KILLER RECEPTOR, NIIBITORY RECEPTOR, IMIBITORY RECEPTOR, 2
\Box	A	536	723	3e-16	000	0.19		MHC CLASS I NK CELL	IMMUNE SYSTEM P58 NATURAL

PDB amotation	OR; KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN	J. IMMUNE SYSTEM PS8 NATURAL OR; KILLER CELL RECEPTOR, KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, IMMUNOGLOBULIN	LI MAUNE SYSTEM PS8 NATURAL 10R; KILLER CELL RECEPTOR, KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN	LI IMMUNE SYSTEM PS8 NATURAL OR; KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBUJIN		AIN: A; IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM		AIN: A; IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM				
Coumpound	RECEPTOR PRECURSOR; CHAIN: A;	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	TO OATO OTTO OTTO
SEQFOL D score												
PMF		0.23	-0.06	-0.06	-0.02	0.27	0.75	0.65	0.65	0.47	0.00	200
Verify		0.20	0.22	0.17	10'0	0.25	0.28	-0.04	0.19	0.38	0.04	900
Psi Blast		3e-21	1.2e-09	5.1e-22	7.5e-15	3.4e-18	7.5e-21	3e-20	1.2e-16	3e-20	3.4e-17	4 50 10
END		256	148	166	349	537	151	536	724	868	666	800
STAR T AA		29	4	813	152	349	37	415	528	740	820	825
CHAI N ID		⋖	∢	<	¥	∢	¥	A	∢	¥	4	V
PDB		2dli	2dli	2dli	2fcb	2fcb	2fcb	2fcb	2fcb	2fcb	2fcb	2fob
SEQ NO: D		1508	1508	1508	1508	1508	1508	1508	1508	1508	1508	1508

PDB annotation	FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM			HYDROLASE PNB ESTERASE; ALPHA-BETA HYDROLASE, DIRECTED EVOLUTION, ORGANIC ACTIVITY, 2 PMB ESTERASE	CHOLINESTERASE SERINE HYDROLASE, NEUROTRANSMITTER CLEAVAGE, CATALYTIC 2 TRIAD, ALPHAIBETA HYDROLASE	HYDROLASE MACHE, HYDROLASE, SERINE ESTERASE, ACETYLCHOLINESTERASE, TETRAMER, 2 HYDROLASE FOLD, GLYCOSYLATED PROTEIN	HYDROLASE BILE SALT ACTIVATED LIPASE, BILE SALT STIMULATED HYDROLASE, SERINE FETIEDA SEF I DA SE
Coumpound		FC GAMMA RIIB; CHAIN: A;	NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGGI (LAMBDA, HIL) 8FAB 3	PARA-NITROBENZYL ESTERASE; CHAIN: A;	ACETYLCHOLINESTERASE; CHAIN: A;	ACETYI.CHOLINESTERASE; CHAIN: A, B, C, D;	CHOLESTEROL ESTERASE; CHAIN: NULL;
SEQFOL D score								
PMF		0.70	0.12	0.47	0.22	0.12	0.43	0.06
Verify		0.00	0.42	0.05	-0.24	-0.23	-0.29	-0.50
Psi Blast		3e-18	1.76-12	5.16-18	9e-13	16-21	5.1e-22	3.4e-19
END		1086	722	529	64	73	73	74
STAR T AA		917	642	353	4	3	6	e .
CHAI N ID		¥	¥	<	A	٧	<	
EDB CI		2fcb	3ncm	8fab	1c7j	lea5	Imaa	2bce
SEQ No id		1508	1508	1508	1510	1510	1510	1510

PDB annotation	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR	PRO REGION PRO REGION, FOLDASE, PROTEIN FOLDING, SERINE PROTFASE	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RALANO), HYDROLASE 2 MOLECULAR RECOGNITION, BEPTOPE MAPPING, LEUCINE-RICH 3 REPRAYS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (RI-MSI), HYDROLASE 2 MOLECULAR RECOGNITION, BPITORE MAPPING, LEUCINE-RICH 3 REPEATS
Coumpound	DNA; CHAIN: A, B, D. E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ADR1; CHAIN: NULL;	ADR1; CHAIN: NULL;	ALPHA-LYTIC PROTEASE; CHAIN: A, B, C;	SYNTAXIN-1A; CHAIN: A, B, C;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D, ANGIOGENIN; CHAIN: B, E;
SEQFOL D score							
PMF	-0.11	0.03	-0.20	-0.19	0.09	1.00	1.00
Verify	0.14.	-0.78	0.09	0.03	-0.01	0.21	0.34
Psi Blast	3.4e-08	5.1e-11	1.7e-11	4.5e-10	4.5e-09	5.1e-25	3c-34
END	274	39	446	166	543	200	469
STAR T AA	241	-	403	81	432	164	243
CHAI N ID	9			A	٧	<	<
සු ය	Imey	2adr	2adr	2pro	lez3	la4y	la4y
SEQ NO:	1512	1512	1512	1514	1515	1521	1521

PDB annotation	COMPLEX (INHIBITORAUCLEASE) COMPLEX (INHIBITORAUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, BETITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (NHIBTIORNUCLEASE) COMPLEX (NHIBTIORNUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, BETIOPE MAPPING, LEUCINE-RICH REPRATS	COMPLEX (THHBITORNUCLEASE) COMPLEX (THHBITORNUCLEASE), COMPLEX (RI-MO), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-MAYO), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH SREPATS	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-
Coumpound	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, B;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C, RAB
SEQFOL D score			113.01				
PMF	1.00	0.95		0.90	0.48	0.39	0.19
Verify	0.51	0.05		-0.03	-0.27	-0.30	0.07
Psi Blast	3e-35	3.4e-24	6.8c-32	6.8e-32	1.2e-23	1.76-21	1.7e-10
END AA	469	407	496	471	438	495	474
STAR	282	7	7	98	267	316	350
CHAI N ID	¥	<	∢	4	V	⋖	v
PDB	la4y	la4y	la4y	la4y	140b	140b	Idee
SEQ NO.	1521	1521	1521	1521	1521	1521	1521

		ä	ä	Z of t	à	20	
PDB annotation	FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	RNA BINDING PROTEIN TAP (NEXI); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	LIGASE CYCLIN A/ODK2. ASSOCIATED PROTEIN P45; CYCLIN A/ODK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LR8, LEUCINE- RICH REBEATI, SCF, UBRQUITIN; 2 E3, UBROUTIN PROTEIN LIGASE	LIGASE CYCLIN ACDR2. ASSOCIATED P45, CYCLIN ACDR2. ASSOCIATED P19, SKP1, SKP2, F. BOX, LRR5, LEUCINE-RICH REPEANS, SCF2, UBGOUTIN, E3, UBIOUTIN PROTEIN LIGASE	CHANGEREPTOR NALIP, ENDIGAP, TOTA ASEA CITYATING PROTEIN PROTEIN, GAP, RANIP, RANIOAP, LRR, LEOCHS, 2 RICH REBEAT TOTA TOTA TOTA TOTA TOTA HEMHEDS ALL TWANNING, HEMHEDS ALL TWANNING, MEROHERNAL TWANNING,	TRANSCRIPTION RNAIP; RANGAP;
Coumpound	GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	SKP2; CHAIN: A, C, B, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P; P, M, P, P, M, P, P, P, M, P, P, P, P, P, P, P, P, P, P, P, P, P,	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	PROTEIN RNAI_SCHPO; CHAIN: A. B;	GTPASE-ACTIVATING
SEQFOL D score					,		
PMF		0.39	0.28	0.03	0.51	0.55	96.0
Verify		-0.04	-0.07	-0.00	80.08	80.0-	0.17
Psi Blast		1.5e-06	1.5e-06	1.7e-12	8.5e-13	6.8e-19	5.1e-21
END		471	471	512	514	814	474
STAR T AA		401	401	254	323	157	215
CHAI N ID		∀	en en	∢	∢	∢ .	<
PDB ID		Igi	161	Ifqv	162	lyrg	lyrg
SEQ NO:		1521	1521	1521	1521	1521	1521

PDB annotation	FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RANGAP, LER, LEICUNE. 2 RICH REPEAT PROTEIN, TWINNING, HEMHEDRA. TWINNING, MEROHEDRA. TWINNING, MEROHEDRA. TWINNING,	GTRASKORPTOWN KHIP, RANGAP, GTRASKA, CHYAATINA PROTEIN GOR, RHI, CTRASKA, CITYATINA RROTBIN, GAP, RIANIP, RANGAP, RROTBIN, GAP, RIANIP, RANGAP, REAGENT, TWANTON, GORDEN, TWANTON, HEMHEDRA, TWYNING, MENCHEDRA, TYWNING, MENCHEDRA, TYWNING,	GTRASCORPTON SKAP, RANGAP; GTRASS-ACTIVATING PROTEIN FOR SPH, CTRASCACTIVATING FOR PROTEIN GAP, RANH P, RANGAP, FREDEN GAP, RANH P, RANGAP, FREDEN TWINNING, FREMEDRA, TWINNING, FREMEDRA, TWINNING, MRROCHERAL TWINNING,	ACETYLATION RNASE INHIBITOR, RIBONUCLEASBANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	ACETYLATION RNASE INHIBITOR, RIBONUCLEASEANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
Coumpound	CHAIN: A, B;	PROTEIN ING PROTEIN INA J. SCHPO; CHAIN: A, B,	PROTEIN RIVAL SCHPO; CHAIN: A, B,	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	RIBONUCLEASE INHIBITOR;
SEQFOL D score				109.97	
PMF		0.55	0.28		0.81
Verify		0.11	0.10		0.12
Psi Blast		4.5e-30	3.4e-09	8.5e-46	8.5e-46
END		469	208	491	511
STAR T AA		243	348	42	68
CHAI		<	A		
E G		lyrg	lyrg	2bnh	2bnh
SEQ B B SE		1521	1521	1521	1521

PDB CHAI STAR END Psi Blast Verify PMF SEQFOL 1D NID TAA AA score score Dscore 1clg A 54 142 4.55c08 0.46 -0.20	END Psi Blast Verify PMF AA score score 142 4.5e-08 0.46 -0.20	Psi Blast Verify PMF score score 4.5e-08 0.46 -0.20	Verify PMF score score 0.46 -0.20	ify PMF re score	G 6)	SEQFOL D score		Coumpound TROPOMYOSIN; CHAIN: A, B,	PDB annotation CONTRACTILE PROTEIN
						Ü	Ü	с, D	TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
50 142 1.5¢-08 0.36 -0.20 CC	142 1.5e-08 0.36 -0.20	1.5e-08 0.36 -0.20	0.36 -0.20	-0.20		ŏ	ŭ	COLICIN IA; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATTON, TRANSMEMBRANE 2 PROTEIN
1ec2 A 50 143 1.1e-12 0.36 -0.14 SV	143 1.1c-12 0.36 -0.14	1.16-12 0.36 -0.14	0.36 -0.14	-0.14		s	S	SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELLX BUNDLE
Ireq A 50 142 4.5e-08 0.11 -0.20 MI	142 4.5e-08 0.11 -0.20	4.5e-08 0.11 -0.20	0.11 -0.20	-0.20		M	22	METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE
1fty B 17 82 1.7e-24 0.78 1.00 SK	82 1.7e-24 0.78 1.00	1.7e-24 0.78 1.00	0.78 1.00	1.00		SK	18 c	SKP2; CHAIN: A, C, E, G, I, K, M,	LIGASE CYCLIN A/CDK2-
5 z		Ź	<u> </u>	ĎŹ	ΰź	δŹ	ΰź	O; SKF1; CHAIN: B, D, F, H, J, L, N, P;	ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19;
									SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITM, 2 E3. UBIOUITIN PROTEIN LIGASE
1fs1 B 17 82 1.7e-24 0.21 0.62 C	82 1.7e-24 0.21 0.62	1.7e-24 0.2I 0.62	0.21 0.62	0.62		0	0	CYCLIN A/CDK2-ASSOCIATED	LIGASE SKP2 F-BOX; SKP1; SKP1,
P V	A A	A d	a d	a 4 0	Z 4 C	- 40	Z ≼ €	A/CDK2-ASSOCIATED P45;	SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3,
152 B 17 82 1.7e-24 0.48 0.99 S	82 1.7e-24 0.48 0.99	1.7e-24 0.48 0.99	0.48 0.99	66.0		S	S	SKP2; CHAIN: A, C; SKP1;	LIGASE CYCLIN A/CDK2-
0	0			0	<u> </u>	<u> </u>	Ü	CHAIN: B, D;	ASSOCIATED P45; CYCLIN A/CDK2-
									ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH
									REPEATS, SCF, 2 UBIQUITIN, E3,
1vcb B 17 80 3.4e-16 0.76 1.00 E	80 3.4e-16 0.76 1.00	3.4e-16 0.76 1.00	0.76 1.00	1.00		H	m	ELONGIN B: CHAIN: A. D. G. J.	TRANSCRIPTION TIMOR
						1 121	ш	ELONGIN C; CHAIN: B, E, H, K;	SUPPRESSOR, CANCER, UBIQUITIN,
							-	VHL; CHAIN: C, F, I, L;	BETA SANDWICH, 2

PDB annotation	DOMAIN, 3 SIGNAL TRANSDUCTION		DOMAIN; PHOSPHOTRANSFERASE,	TPASE ACTIVATING PROTEIN, GAP,	CDC42, 2 PHOSPHOINOSITIDE 3-	KINASE, SH3 DOMAIN, SH2	DOMAIN, 3 SIGNAL	TRANSDUCTION	G-PROTEIN CDC42 GTPASE-	ACTIVATING PROTEIN; G-PROTEIN,	GAP, SIGNAL-TRANSDUCTION	G-PROTEIN CDC42 GTPASE-	ACTIVATING PROTEIN; G-PROTEIN,	GAP, SIGNAL-TRANSDUCTION	G-PROTEIN CDC42 GTPASE-	ACTIVATING PROTEIN; G-PROTEIN,	GAP, SIGNAL-TRANSDUCTION	COMPLEX(GTPASE		GTPASE-ACTIVATING PROTEIN	RHOGAP; COMPLEX (GTPASE	ACTIVATION/PROTO-ONCOGENE),	GTPASE, 2 TRANSITION STATE, GAP			GTPASE-ACTIVATING PROTEIN	RHOGAP; COMPLEX (GTPASE	ACTIVATION/PROTO-ONCOGENE),	GTPASE, 2 TRANSITION STATE, GAP	COMPLEX(GTPASE		CITAL STATE OF LANCE AND LANCE OF THE STATE
Coumpound		PHOSPHATIDYLINOSITOL 3-	KINASE; CHAIN: A, B;						RHOGAP; CHAIN: NULL;			RHOGAP; CHAIN: NULL;			RHOGAP; CHAIN: NULL;			P50-RHOGAP; CHAIN: A;	TRANSFORMING PROTEIN	RHOA; CHAIN: B;				P50-RHOGAP; CHAIN: A;	TRANSFORMING PROTEIN	RHOA; CHAIN: B;				P50-RHOGAP; CHAIN: A;	PHOA: CHAIN: D:	
SEQFOL D score															94.76															107.06		
PMF		0.95							1.00			0.54						1.00						1.00								
Verify		0.44		_	_				0.77			80.0						0.88						0.18								
Psi Blast		3e-36							1.5e-37			1e-29			1.5e-37			7.5e-39						1.7e-29						7.5e-39		
END		311							308			27.7			308			308						304						308		_
STAR T AA		125							112			88			88			112						16						91		
CHAI N ID		В																¥						٧						4		
PDB ID		Ipbw							lrgp			lrgp			Irgp			ltx4						ltx4						1tx4		
SEQ NO:		1524							1524			1524			1524			1524						1524						1524		_

PDB annotation	ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME	LIGASE E6AP, UBCH7, BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME	LIGASE UBIQUITIN, UBIQUITIN- CONJUGATING ENZYME, YEAST	LIGASE UBIQUITIN, UBIQUITIN- CONJUGATING ENZYME, YEAST	UBIQUITIN-CONUGATING ENEYME UBIQUITIN- CONUGATING ENZYME; UBIQUITIN-CONUGATING ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN- CONJUGATING ENZYME; UBIQUITIN-CONJUGATING
Coumpound		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	UBC9; CHAIN: NULL;	UBC9; CHAIN: NULL;
SEQFOL D score		92.22			80.53		106.20		73.11
PMF			1.00	66'0		1.00		0.1	
Verify score			0.61	0.36		0.57		0.83	
Psi Blast		1e-40	le-40	8.5e-33	8.50-33	3.4e-51	3.4e-51	3.4e-38	3.4e-38
END		134	128	129	129	130	131	130	131
STAR T AA		_	4	s	S	_	4	-	-
CHAI N ID		¥	<	Д	Q	A	A	A	V
EDB ID		layz	layz	lo4z	104z	Ided	1qcq	Iu9a	1u9 a
SEQ NO:		1525	1525	1525	1525	1525	1525	1525	1525

PDB annotation	ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE	UBIQUITIN CONJUGATION UBCI; UBIQUITIN CONJUGATION, LIGASE	UBIQUITIN CONJUGATION UBCI; UBIOUITIN CONJUGATION, LIGASE	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) MOLECULAR RECOGNITION, BRITORE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (INHIBITOR/NUCLEASE), MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
Coumpound		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN; NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	KIBONUCLEASE INHIBITOR; CHAIN: A, D, ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;
SEQFOL D score		96.00		82.57		77.96			67.17
PMF			1.00		1.00		1.00	0.03	
Verify			0.49		0.66		0.80	-0.14	
Psi Blast		1.2c-4I	1.2e-41	1.5e-37	I.5e-37	1.7e-36	1.7e-36	5.1e-19	3.4e-18
END		126	127	132	124	132	128	338	473
STAR T AA		_	_	_	e	7	en .	10	10
CHAI N ID								V	<
PDB		2aak	2aak	2e2c	2e2c	2ncz	2ucz	Ia4y	Ia4y
SEQ No in		1525	1525	1525	1525	1525	1525	1527	1527

PDB annotation	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (ILAND, HYDROLASE 2 MOLECULAR RECOGNITION, BETTOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (INHIBITOR/NUCLEASE), MOLECULAR RECOGNITION, EBTTOPE MAPPING, LEUCNE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (EL-AND, HYDROLASE 2 MOLECULAR RECOGNITION, EBITOPE MAPPING, LEUCNE-RICH 3 REPEATS	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
	CON COM MOL BPIT	CON COM MOL EPIT	CON COM MOL BPIT	PRO SNR	PRO (NUC SNR	PRO SNE	PRO
Coumpound	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, B;	NIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	U2 RNA HARPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A; CHAIN: A, C; UZ B"; CHAIN: B, D;	UZ RNA HARPIN IV; CHAIN: Q, R; UZ A; CHAIN: A, C; UZ B°; CHAIN: B, D;	UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A'; CHAIN: A, C; UZ B"; CHAIN: B, D;
SEQFOL D score							
PMF	0.68	0.76	0.99	0.60	0.01	0.22	0.13
Verify	0.07	0.27	0.36	0.50	0.25	0.36	0.18
Psi Blast	9e-28	3.46-18	1.5e-34	3e-25	7.5e-24	1.5e-14	3.4e-07
END	335	415	309	284	291	326	339
STAR T AA	134	25	99	140	164	212	232
CHAI N ID	∢	∢	∀	V	∢	٧	A
EDB CI	la4y	la4y	la4y	la9n	la9n	1a9n	la9n
SEQ B SEQ	1527	1527	1527	1527	1527	1527	1527

				,			,		
PDB annotation	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONICLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONLICLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONICLEOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX
Coumpound	 	UZ RNA HAIRPIN IV; CHAIN: Q. R; UZ A'; CHAIN: A, C; UZ B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A; CHAIN: A, C; UZ B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	UZ RNA HAIRPIN IY; CHAIN: Q. R; UZ A'; CHAIN: A, C; UZ B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q. R; U2 A'; CHAIN: A, C; U2 B";
SEQFOL D score									
PMF	0.68	0.98	0.43	0.45	0.27	0.00	0.43	0.96	0.70
Verify	0.42	0.15	0.23	0.25	0.37	0.03	0.36	0.37	0.16
Psi Blast	1.7e-07	1.5e-24	3e-26	4.5e-26	9e-15	3.4e-05	1.7e-07	3e-24	le-24
END	146	187	234	290	326	25	146	187	215
STAR T AA	43	51	26	140	212	23	43	21	89
CHAI	¥	<	¥	ပ	ပ	υ	o	υ υ	၁
10 B	la9n	la9n	la9n	la9n	la9n	la9n	la9n	la9n	la9n
SEQ NO ID	1527	1527	1527		1527	1527	1527	1527	1527

PDB annotation	(NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,	STANDARY OF THE STANDARY OF THE REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL STRUCTURE, KAB GERANYLGERANT, TRANSFERASE, 20 A 2 RESOL, TTON, IN- FORMYLAETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNGIN, 2 CHLAMYDOMONAS, FLAGELLA	CONTRACTLE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
Coumpound	CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN; A; .	RAB GERANYLGERANYLIRANSFE GERANYLGERANYLIRANSFE CHAIN: A, C; RAB GERANYLGERANYLIRANSFE RASE BETA SUBUNIT, CHAIN: B, D;	OUTER ARM DYNEIN; CHAIN: A;	OUTER ARM DYNEIN; CHAIN: A;	OUTER ARM DYNEIN; CHAIN: A;
SEQFOL D score									
PMF		69.0	0.99	0.10	0.70	0.15	90'0	-0.09	0.23
Verify		0.43	0.35	-0.07	0.12	0.31	-0.40	0.12	-0.08
Psi Blast		3e-26	8.5e-24	3.4e-18	3.4e-23	1.26-10	1.5e-18	5.16-15	ie-09
END		234	311	377	881	121	291	338	145
STAR T AA		92	129	228	4	21	167	217	43
CHAI N ID		2	4	4	∢	A	¥	V	∢
EDB CII		la9n	140b	1406	1406	ldoe	1ds9	1ds9	1489
SEQ ID NO:		1527	1527	1527	1527	1527	1527	1527	1527

PDB annotation	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP, RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (J.RR)	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	LIGASE CYCLIN A/CDK2. ASSOCLATED PROTEIN V45; CYCLIN ACDK2-ASSOCLATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- SKP1, SKP2, F-BOX, LRR, LEUCINE- SK D19 SWP1, SKP3, SWP1,	LIGASE CYCLIN A/CDK2- ASSOCIATED PS; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF3, LUBQUITIN, E3, UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2. ASSOCIATED P45, CYCLIN A/CDK2. ASSOCIATED P19; SKP1, SKP2, F. BOX, LRRS, LEUCINE-RICH REPEATS, SCF2, USBQUITIN, E3, UBIQUITIN PROTEIN LIGASE.	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP,
Coumpound	OUTER ARM DYNEIN; CHAIN: A;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	SKP2, CHAIN: A, C, B, G, I, K, M, O, SKP1; CHAIN: B, D, F, H, J, L, N, P,	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;
SEQFOL D score							
PMF	0.15	0.01	0.30	0.36	-0.03	0.04	-0.03
Verify	-0.39	-0.15	0.16	-0.05	0.21	0.00	0.16
Psi Blast	1.46-11	3.4e-07	3.40-07	1.5e-15	1.36-20	5.10-12	6.8e-12
END	235	308	308	347	334	311	360
STAR T AA	73	227	227	134	125	171	29
CHAI	<	∢	я	4	₹ ,	<	Ą
90g en	1ds9	161	I61	Ifqv	1152	1162	lyrg
SEQ	1527	1527	1527	1527	1527	1527	1527

					-T		т	
PDB annotation	LRR, LEUCINE- 2 RICH REPEAT RKOTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRAY	MANSCHEUTON KNA IP, RANGAP, OTP ASE-ACTIVATING PROTEIN OF SEIT, OTPAS ASE-ACTIVATING PROTEIN, OAP, RANDIR, RANGAP, LIRA, LBUCTING, 2 RICH RETEAST PROTEIN, TWINNING, HEMHEDBAL, TWINNING, 3 MEROHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, 3	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	POTASSIUM CHANNELS, POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X- RAY 2 STRUCTURE, APLYSIA KV1.1	SIGNALING PROTEIN VOLTAGE- GATED POTASSIUM CHANNEL, ASSEMBLY DOMAIN, TETRAMER	METAL TRANSPORT ION CHANNEL, OXIDOREDUCTASE, BETA SUBUNIT	SIGNALING PROTEIN VOLTAGE.
Coumpound		PROTEIN RATIVATING PROTEIN RIVAL SCHPO; CHAIN: A, B;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	POTASSIUM CHANNEL KVI.1; CHAIN: NULL;	KVI.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D, E, F, G, H;	KV BETAŽ PROTEIN; CHAIN: A; POTASSIUM CHAINBL KV1.1; CHAIN: E;	KV1.2 VOLTAGE-GATED
SEQFOL D score								
PMF		0.15	0.74	0.81	0.86	0.28	0.41	0.43
Verify score		0.11	80.0	10:0	99:0	60'0	0.48	0.48
Psi Blast		16-30	1.26-22	1.2e-40	1.5e-13	7.50-12	1.26-11	3e-12
END AA		265	413	312	207	504	210	208
STAR T AA		98	25	64	1117	117	1117	117
CHAI N ID		∢				∢	ы	¥
EDB OI		lyrg	2bnh	2bnh	1a68	Idsx	lexb	Iqdv
SEQ OO:		1527	1527	1527	1528	1528	1528	1528

PDB annotation		GATED POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, 2 INTRACELLULAR GATE, TETRAMER	PROTON TRANSPORT POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-RAY STRUCTURE, 2 APL YSIA KV11, PROTON TRANSPORT	POTASSIUM CHANNEL POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, MOLECULAR 2 RECOGNITION, ZINC-BINDING	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER		GUANING NUCLEOTIDE EXCIANGE FACTOR ROCK; GUANNING NUCLEOTIDE EXCITANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TTRY	GUANINE NUCLEOTIDE EXCHANGE FACTOR ROCT, GUANNINE. NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER	GENE REGULATION SON OF SEVENLESS PROTEIN; GUANINE
		GATED POT TETRAMERI INTRACELL TETRAMER	PROTON TRA CHANNELS, 1 DOMAIN, X-R APLYSIA KVI TRANSPORT		GUANINE FACTOR R NUCLEOTI GEF, RAN, GTP BINDI	TER	GUANINE FACTOR R NUCLEOTI GEF, RAN, GTP BINDI TER	GUANINE FACTOR R NUCLEOTI GEF, RAN, GTP BINDI	GENE REG SEVENLES
Coumpound	1	POTASSIUM CHANNEL; CHAIN: A, B, C, D;	POTASSIUM CHANNEL KVI.I; CHAIN: A;	POTASSIUM CHANNEL PROTEIN SHAW; CHAIN: NULL;	REGULATOR OF CHROMOSOME CONDENSATION 1; CHAIN: A, B, C;		REGULATOR OF CHROMOSOME CONDENSATION I; CHAIN: A, B, C,	REGULATOR OF CHROMOSOME CONDENSATION I; CHAIN: A, B, C,	HUMAN SOS 1; CHAIN: A;
SEQFOL	D score						97.41		
PMF	score		0.45	0.62	-0.08			0.22	0.22
Verify	score		0.26	0.39	0.04			-0.01	-0.03
Psi Blast			1.3e-11	6e-15	1.7e-49		1.7e-49	6.8e-91	3e-16
END	¥.		204	217	704		741	415	1001
STAR	I AA		117	117	346		354	6	695
CHAI	3	_	∢		4		٧	A	A
PDB	1		ptit	3kvt	lal2			1a12	1dbh
SEQ	ö		1528	1528	1529		1529	1529	1529

PDB annotation	NUCLEOTIDE EXCHANGE FACTOR, GENE REGULATION	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL	TRANSDUCTION PROTEIN, ADAPTOR PROTEIN	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-	PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN,	ADAPTOR PROTEIN					SIGNAL TRANSDUCTION SON OF SEVENLESS, PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN-	BINDING PROTEIN, POLY-L-2	PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN-
Coumpound		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-	CHAIN: A;		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL	DOMAIN) MUTANT IPLS 3	WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4	(INS(G105-LEHHHHHH)) (NMR, 25 STRUCTURES) IPLS 5	SOS 1; CHAIN: NULL;	PROFILIN II; CHAIN: A, B, C, D;			PROFILIN II; CHAIN: A, B, C, D;
SEQFOL D score															
PMF score		0.33		0.35			0.93				-0.02	1.00			1.00
Verify score		-0.27		0.02			0.38				0.32	1.32			1.32
Psi Blast		7.5e-07		3e-07			0.0003				1.5e-09	6.8e-52			9e-63
END		1006		1007			1007				1004	138			138
STAR T AA		930		930			935				897	7			2
CHAI		¥		V								¥.			٧
PDB CI		Ifao		1fb8			lpis				Ipms	ig j			IdIj
S e S		1529		1529			1529				1529	1530			1530

PDB annotation	BINDING PROTEIN, POLY-L- 2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN	PROTEIN BINDING ACETYLATION, ACTIN-BINDING PROTEIN, MULTIGENE PAMILY	PROTEIN BINDING ACETYLATION, ACTIN-BINDING PROTEIN, MULTIGENE FAMILY			CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN-BINDING PROTEIN, POLY-L- 2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOCORM, ACTIN- BRIDING PROTEIN, POLY-1 2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN				MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTIBILE
Coumpound		PROFILIN; CHAIN: NULL;	PROFILIN; CHAIN: NULL;	ACTIN BINDING PROTEIN PROFILIN IPNE 3	ACTIN BINDING PROTEIN PROFILIN 1PNE 3	PROFILIN II; CHAIN: A, B, C, D;	PROFILIN II, CHAIN: A, B, C, D,	ACTIN BINDING PROTEIN PROFILIN 1PNE 3	ACTIN BINDING PROTEIN PROFILIN 1PNE 3		KINESIN; CHAIN; NULL;	KINESIN; CHAIN: NULL;
SEQFOL D score			167.69		167.40				133.14			
PMF		00.1		1.00		1.00	0.1	1.00			0.1	1.00
Verify		1.04		0.92		0.75	0.71	0.64			-0.22	-0.15
Psi Blast		1.7e-52	1.7e-52	1.7e-52	1.7e-52	1.7e-42	4.5e-52	1.5e-42	1.5e-42		36-68	6.8e-35
END		140	140	140	140	22	122	124	124	1	176	941
STAR		2	2	2	2	61	2	2	2		7	2
CHAI N ID						∢	⋖					
PDB ID		161	161	lpne	Ipne	141	1415	lpne	Ipne		1bg2	1bg2
SEQ NO.		1530	1530	1530	1530	1531	1531	1531	1531	100	1534	1534

PDB annotation	ASSOCIATED		PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE	MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN,	+	MICROTUBULE-BASED MOTOR,	+	CONTRACTILE PROTEIN, KAR3,	KINESIN-RELATED PROTEIN,	MOTOR 2 PROTEIN, ATPASE, P-	LOOP, MICROTUBULE BINDING	MOTOR PROTEIN MOTOR PROTEIN,	CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	SF					-	A: AMINOTRANSFERASE, PYRIDOXAL
Coumpound		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C,	ć.		KINESIN; CHAIN: A, B;	KINESIN; CHAIN: A, B;	KINESIN MOTOR NCD; CHAIN:	· Y;	KINESIN-LIKE PROTEIN KAR3;	CHAIN: NULL;			-	KINESIN HEAVY CHAIN;	CHAIN: A, B, C, D;	KINESIN HEAVY CHAIN; CHAIN: A. B. C. D:	TRANSFERASE(AMINOTRANSF	ERASE) ASPARTATE AMINOTIR ANSFER A SE	(E.C.2.6.1.1) COMPLEXED WITH	1ARS 3 PYRIDOXAL-5-	PHOSPHATE LARS 4	ASPARTATE	AMINOTRANSFERASE; CHAIN:
SEQFOL D score																							
PMF		0,10			0.83	1.00	0.54		9970					86.0		0.71	0.07					0.75	
Verify score		-0.36			0.03	-0.17	-0.24		-0.30					-0.25		-0.44	-0.22					0.17	
Psi Blast		le-17			3e-40	6.8c-19	6.8e-18		1.7e-21					1.5e-38		1.7e-20	6.8e-13					5.1e-81	
END		6			186	199	170		172					186		230	369					369	
STAR T AA		4			101	101	4		-					105		105	11					_	
CHAI		٧			В	м	A							п		В						٧	
en Bar		lcz7			2kin	2kin	2ncd		3kar					3kin		3kin	lars					1bjw	
SEQ NO EQ	-	1534			1534	1534	1534		1534					1534		1534	1536					1536	

PDB annotation	TIGANSTERASE AONS, S-AMINO-7- KETOPELAGONATI SYNTHASE; PLP-DEPRIDENT ACTL-COA SYNTHAGE, BOTTON BIOSYNTHESIS, 8-2 AMINO-7-CXCNANNO-TE SYNTHASE, BOTTON KETOPELAGONAATE SYNTHASE, TROPELAGONAATE SYNTHASE, TRANSTERASE	TIGANERASE ANDS, SAMING-7- KETOPELARGONATE SYNTHASE; TAP-DEPENDENT ACTL-COA SYNTHASE, BOTTN BIOSYNTHESIS, 8-2 AMINO-7-COXONANOATE SYNTHASE, SOFTOPELARGONATE SYNTHASE, STOPELARGONATE SYNTHASE, TRANSPERASE	TRANSFERASE TAT; TYROSINE N: CATABOLISM; TRANSFERASE, AMINOTRANSFERASE, 2 PYRIDOXAL-S-PHOSPHATE; PLP		TRANSFERASE AMINOTRANSERASE FOLD, LARGE PLP-BINDING DOMAIN, SMALL C: 2 TERMINAL DOMAIN, OPEN ALPHA-BETS STRUCTURE.	LYASE DGD; ENZYME COMPLEXES, CATALYTIC MECHANISM, DECARBOXYLATION 2 INHIBITOR, LYASE	LYASE DGD; ENZYME COMPLEXES, CATALYTIC MECHANISM.
Coumpound	&AMINO-1-OXONANOATE SYNTHASE, CHAIN. A;	&AMINO-J-OXONANOATE SYNTHASE, CHAIN: A,	TYROSINE AMINOTRANSFERASE; CHAIN: A, B;	CYSTALYSIN; CHAIN: A, B, C, D, E, F, G, H;	MALY PROTEIN; CHAIN: A, B,	2,2-DIALKYLGLYCINE DECARBOXYLASE (PYRUVATE); CHAIN: A;	2,2-DIALKYLGLYCINE DECARBOXYLASE
SEQFOL D score	69.72					169.86	
PMF		0.12	0.16	0.25	-0.05		1.00
Verify score		0.32	60'0	-0.03	0.10		0.72
Psi Blast	1.7e-41	1.7e-41	6.80-54	1.7e-18	3.46-21	3.4e-63	3.4e-63
END	375	365	373	373	373	372	372
STAR T AA	_	47	_	89	26	_	46
CHAI	4	∢	A	V	¥	∢	<
FDB TD	1650	1650	1bw0	lc7n	1d2f	1d7u	1d7u
SEQ NO DE	1536	1536	1536	1536	1536	1536	1536

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PDB annotation	AMINOTRANSFERASE, 5- FLUOROMETHYLORNITHINE, PLP- DEPENDENT 2 ENZYME, PYRIDOXAL PHOSPHATE	HYDROLASE SERCA!; ION PUMP. CALCIUM, MEMBRANE PROTEIN, P- TYPE ATPASE, ACTIVE 2 TRANSPORT		HYDROLASE TETRATRICOPEPTIDE, TRP: HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	SIGNALLING COMPLEX RACI; PS7PHOX, SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	Terraphorate and any and and a state
Coumpound	AMINOTRANSFERASE; CHAIN: A, B, C;	CALCUM-TRANSPORTING ATPASE SARCOPLASMIC CHAIN: A;		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1: CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	TPRZA-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPRZA-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEBVD; CHAIN: B;	TEP A DOMAIN OF HOB.
SEQFOL D score									
PMF		0.04		0.77	0.15	0.29	0.54	0.19	0.50
Verify		-0.16		0.06	-0.35	-0.12	0.21	0.00	92.0
Psi Blast		0		3.46-23	1e-10	1.56-13	Ie-12	le-18	10-18
END		916		247	253	230	196	231	167
STAR T AA		16		135	179	102	101	139	67
CHAI		4				В	Ą	∢	4
808 01		leal		1a17	1a17	9691	lelr	lelr	leir
SEQ No. 19		1539		1541	1541	1541	1541	1541	1541

								,	·
PDB annotation	PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMFLEX, TETRAL RICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT	PROTEIN TRANSPORT HELIX- TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT	TRANSFERASE METHYLTRANSFERASE	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN.
Coumpound	CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR I-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR, CHAIN: A, B, PTSI-CONTAINING PEPTIDE, CHAIN: C, D,	VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	GLYCINE N- METHYLTRANSPERASE; CHAIN: A, B, C, D;	MJ0882; CHAIN: A;
SEQFOL D score							63.04		
PMF		0.53	0.01	0.46	0.37	0.18		-0.09	0.37
Verify		-0.04	0.30	0.73	0.35	-0.06		0.55	0.57
Psi Blast		1.7e-20	3.4e-15	le-14	3.4e-13	8.5e-35	3.4e-07	3.4e-16	3.4e-09
END		250	133	5/1	202	252	254	190	187
STAR T AA		133	28	64	86	9	2	92	72
CHAI N ID		¥	Ą	∢	∢	¥	4	٧	¥.
808 E1		lelw	lelw	Telw	lelw	1feh	Idde	1d2h	1dus
SEQ NO EQ		1541	1541	1541	1541	1541	1541	1542	1542

							I	
PDB annotation			COMPLEX (DNA-BINDING PROTEINDINA) GHF-1; COMFLEX (DNA-BINDING PROTEIN/DNA), PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	PROTEINDNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	TRANSCRIPTION/DNA UJINBARTIORAKA; BER PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY	TRANSCRIPTIONDNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS.
Coumpound	IAHD 4 16 STRUCTURES) 1AHD 5	ANTENNAPEDIA PROTEIN ANTENNAPEDIA PROTEIN (HOMEDDOMAND) MUTTANT WITH CYS 30 HALBD 3 REPLACED BY SER (C595) COMPLEX WITH DNA (NMR, 1 AHD 4 16 STRUCTURES) 1AHD 5	PIT-1; CHAIN: A, B; DNA; CHAIN: C, D;	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	HOMEOBOX PROTEIN HOX-BI; CHAIN: A; PBXI; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	HOMBOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN 4; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5:-CHAIN: C; DNA (5:- CHAIN: D;	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B;
SEQFOL D score				78.21			55.32	
PMF		1.00	0.59		00:1	1.00		1.00
Verify		0.01	-0.40		0,40	0,40		0.49
Psi Blast		5.1e-32	4.5e-22	3e-28	3e-28	5.1e-26	5.1e-27	5.1e-27
END AA		294	586	290	290	290	287	287
STAR		229	212	224	233	233	226	233
CHAI		e.	<	∢	Ą	A	∢	⋖
PDB ID		lahd	Iau7	1672	1672	1672	ib8i	Ib8i
SEQ NO:		1545	1545	1545	1545	1545	1545	1545

PDB annotation		AA (5'- DEVELOPMENT, 2 SPECIFICITY	TARAZU MAIN) S) IFTZ 3	TARAZU MAIN) S) IFTZ 3	TEIN TANT ND ND DD (NNR, 20	INN TRANT TANT (MAR, 20	TEIN; COMPLEX (DNA-BINDING IAIN: C, PROTEIN/DNA) HD; HOMEDOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)		
Coumpound		DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) CNMB. 20 STRUCTURES) 1FTZ 3	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR. 20 STRUCTURES) (FTZ 3	DNA-BINDING PROTEIN ANTENANDEDA PROTEIN (HOMEODOMAIN) MITHANT WITH CYS 39 ISAN 3 WITH CYS 39 ISAN 3 WEBLACED B YEBR AND RESIDUES 1-6 DELETED (CS9S,DEL 1-6) ISAN 4 (NMR, 20	TATIOC I DORAS I PRANT 3 DNA-BINDING PROTEIN ANTENNAPEDIA RECITEIN WITH CYS 39 ISAN 3 WITH CYS 39 ISAN 3 WITH CYS 39 ISAN 3 WITH CYS 39 ISAN 3 WITH CYS 39 ISAN 3 WITH CYS 39 ISAN 3 WITH CYS 39 ISAN 3 WITH CYS 39 ISAN 3 WITH CYS 39 ISAN 3 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 4 WITH CYS 30 ISAN 5 WITH CYS 30 ISAN	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	
SEQFOL	D score		59.53		57.26			61.44	
PMF	score			0.92		1.00	1.00		
Verify	score			-0.12		0.30	0.42		
Psi Blast			8.5e-28	8.5e-28	1.4e-29	1.4e-29	1.7e-29	1.7e-29	
END			296	294	291	294	288	288	
STAR	TAA		227	229	234	235	233	233	
CHAI	e Z						∢	∢	
PDB	A		T#I	1ftz	Isan	Isan	9ant	9ant	
SEO	Βÿ		1545	1545	1545	1545	1545	1545	

Coumpound PDB annotation	CHAIN: A; DUPLEX COMPLEX (ZINC FINGERIDING) OLIGONUCLEOTIDE BINDING ZINC FINGER, DNA-BINDING SITE; CHAIN: B, C; PROTEIN	QGSR ZINC FINGER PEFTIDE; COMPLEX (ZINC FINGER/DNA) CHAIN: A; DUPLEX COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) SITE: CHAIN: B. C: PROTEIN	GGSR ZINC FINGER PEFTIDE; COMPLEX (ZINC FINGER/DNA) CHAIN: A; DUPLEX COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) SITTS: CLEATURE BINDING PROTEIN PROTE	QGSR ZINC FINGER PEFTIDE; COMPLEX (ZINC FINGER/DNA) CHAIN: A: DUPLEX COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) SITTS. CHAIN: B, C; PROTEIN	QGSR ZINC FINGER PEFTIDE; COMPLEX (ZINC FINGER/DNA) CHAIN: 4; DUPLEX COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) SITTE, CHAIN: 8, C; PROTEIN	QGSR ZINC FINGER PEPTIDE; COMPLEX (ZINC FINGER/DNA) CHAIN: A) DUPLEX COMPLEX (ZINC FINGER/DNA) OLGON/LICLEOTIDE BINDING ZINC FINGER, DNA-BINDING STIT: CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; COMPLEX (ZINC FINGER/DNA) CHANN: 4, DUPLEX COMPLEX (ZINC FINGER/DNA) OLIGON/UCLEOTIDE BINDING ZINC FINGER, DNA-BINDING STITE, CHAINE, B. C.	DNA; CHAIN: A, B, D, E; COMPLEX (ZINC FINGER/DNA) ZINC
CHAIN: A; DI OLIGONUCLI SITE; CHAIN: QGSR ZINC F	QGSR ZINC F	OLIGONUCE, SITE; CHAIN	QGSR ZINC F CHAIN: A; DU OLIGONUCL SITE; CHAIN:	QGSR ZINC F CHAIN: A; DI OLIGONUCL SITE; CHAIN	QGSR ZINC F CHAIN: A; DI OLIGONUCLI SITE; CHAIN:	QGSR ZINC F CHAIN: A; DU OLIGONUCLI SITE; CHAIN:	QGSR ZINC F CHAIN: A; DI OLIGONUCLI SITE; CHAIN:	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
							80.58	
Score		1.00	0.88	00'1	0.80	1.00		0.23
verity score		0.26	0.16	0.48	0.31	0.22		0.01
Psi Blast		8.5e-27	3e-28	1.5e-37	5.1e-22	3.4e-30	3.4e-30	1.5e-14
END		249	250	277	25	361	391	281
STAR T AA		161	162	199	-	281	309	101
CHAI		V	<	∢	Y	∢	4	c
2 E		laīh	lalh	lalh	lalh	lalh	laih	Imey
S E S		1546	1546	1546	1546	1546	1546	1546

SEQ B D SE	PDB ID	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	Imey	၁	125	249	6e-25	-0.12	0.49		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (7TNC FINGER FINA)
1546	Imey	ပ	130	221	1.5e-39	-0.10	0.48		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (77NC FINGER/DNA)
1546	Ітеу	ပ	160	249	5.1e-47	0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	Imey	o	188	277	1.76-47	0.57	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	Ітеу	ပ	-	42	5.1e-34	0.26	0.95		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	lmey	၁	224	305	1e-49	0.81	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1546 Imey C	ပ	224	306	1e-49			105.23	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

PDB annotation	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGERDNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGERDNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRETTON REGULATIONINNA) COMPLEX (TRANSCREPTON REGULATIONINNA), RNA POLYMERASE III, 2 TRANSCRETTON INTIATION, ZINC FRANSCRETTON INTIATION, ZINC	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION
Coumpound	CONSENSUS ZINC FINGER PROTEIN; CHAIN; C, F, G,	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, B; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, B; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TFIIIA, CHAIN: A, D, 3S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;
SEQFOL D score							117.50
PMF		1.00	1.90	1.00	00:1	0.46	
Verify score		0.59	0.38	0.37	0.26	0.03	
Psi Blast		1.26-49	3.46-49	1.26-49	3.46-44	1.4e-31	1.5e-37
END		333	361	389	411	291	359
STAR		252	280	308	336	132	961
CHAI N ID		ပ	o	ပ	ပ	<	V V
PDB		Imey	Imey	Imey	Imey	1416	1tf6
SEQ No de		1546	1546	1546	1546	1546	1546

	NC NC	NC	, QC	NC	12 1	
PDB annotation	REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMENASE III, 2 TRANSCRIPTION, INITIATION, ZINC TRANSCRIPTION INITIATION, ZINC	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMENASE III, 2 TRANSCRIPTION, INITATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/MA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC TRANSCRIPTION INITIATION, ZINC	COMPLEX (TRANSCRIPTION INTERNSCRIPTION INTERNSCRIPTION INTITATION, INTITATION, INTITATION, INTITATION, INTITATION, INTITATION, INTITATION, INTITATION, INTITATION, INTITATION, INTITATION, IS COMPLEX (TRANSCRIPTION), IS COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCRIPTION
	2245	SEESE	886884	SEESE	SERINESES	ပ္
Coumpound	-	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S KIBOSOMAL, RNA GENE; CHAIN: B, C, E, F;	TFIIA; CHAIN: A, D; 5S RIBOSOMAL, RNA GENE; CHAIN: B, C, E, F;	YYI; CHAIN: C; ADENO. ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO-
SEQFOL D score						
PMF score		1.00	8.1	57.0	0:00	66.0
Verify score		0.41	0.32	0.07	0.20	0.28
Psi Blast		1.5e-37	1.5e-37	1.7e-26	6.8e-31	3e-40
END		342	403	410	249	277
STAR T AA		199		309	133	165
CHAI N ID		∢	<	∢	S	၁
PDB ID		11(6	1476	1476	1ubd	1546 lubd C
SEQ No: D		1546	1546	1546	1546	1546

		r			
PDB annotation	REGILATION/DNA) YING-YANG 1; TRANSCEPTION INITIATION, INITIATION, ELEMENT, YYL, ZINCZ FINGER PROTEIN, DINA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCEPTION)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA, PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCRETTION REGULATION/DNA) TYNG-YANG I; TRANSCRETION INITIATION, INITIACON, ELEMENT, YY1, ZINCZ FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRETION)	COMPLEX (TRANSCRIPTION REGILATION/DAY) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION
Coumpound	ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YY; CIAIN: C; ADBNO- ASSICIATED VIRUS P; INITIATOR ELEMENT DNA; CHAIN: A, B;	YYY; CIAIN: C; ADENO- ASSOCIATED VIRUS P\$ INITATOR ELEMENT DNA; CHAIN: A, B;	ASSOCIATION C, ADENO- ASSOCIATION VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA:
SEQFOL D score					
PMF		1:00	0.81	0.16	1.00
Verify		0.47	0.24	-0.28	-0.01
Psi Blast		5.1e-33	3e-25	1.7e-23	3.4e-29
END		277	611	150	35
STAR		168	16	61	
CHAI N ID		o	o	၁	c
PDB ID		1ubd	lubd	1ubd	lubd
SEQ ID NO:		1546	1546	1546	1546

		1	_										_			
PDB annotation	INITIATOR ELEMENT, YYI, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATIONDNA)	COMPLEX (TRANSCRIPTION REGULATIONDNA) YING-YARG 1; TRANSCRETTON INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DIAA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION,	INITIATOR BLEMENT, YYI, ZINC 2	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGIII ATTOMONA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG I;	TRANSCRIPTION INITIATION,	FINGER PROTEIN DNA-PROTEIN
Coumpound	CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED YIRUS PS INITIATOR ELEMENT DINA; CHAIN: A, B;		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	CHAIN: A, B;			YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA;	CHAIN: A, B;			YYI; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CEAIN: A, B;
SEQFOL D score				97.53												
PMF		8.						00'I					1.00			
Verify score		0.25						0.44					0.42			
Psi Blast		7.5e-48		1.2e-50				1.2e-50					4.5c-47			
END		333		334				362					389			
STAR T AA		201		226				250					279			
CHAI N ID		v		c				ပ					o			
PDB		Iubd		Iubd				Inbd					lubd			
SEQ NO ID		1546		1546				1546					1546			

PDB annotation	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)		INTIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)			RECOGNITION, 3 COMPLEX (TRANSCRIPTION			FINGER PROTEIN, TY1, ZINCZ	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGIII ATTOMONA)		OWL)	3)	NEP 3	
L Coumpound		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	CHAIN: A, B;		ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;		COMPLEX(TRANSCRIPTION REGIT ATTONONA)	TRAMTRACK PROTEIN (TWO	ZINC-FINGER PEPTIDE)	DNA 2DRP 4	
PMF SEQFOL score										_					-
Verify PN score sco		0.35 1.00		0.11 1.00		-	0.16 0.93				0.24 0.74	_			
Psi Blast		1.76-33		7.5e-46			8.5e-32 (16-10				
END		389		417			410				122				9
STAR T AA		288		306			316				8				
CHAI N ID		υ		၁			Ü				٧				-
PDB UI		Iubd		1ubd			Inpq				2drp				
SEQ No us		1546		1546			1546				1546				1647

PDB CHAI STAR END ID NID TAA AA	STAR	_	AA EN		Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB amotation
									CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
2gii A 137 248 3.4e-26	248	248		3.4e-26		-0.08	0.34		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEINIDNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN(DNA)
2gli A 160 304 3.46-32	304	304		3.4e-32		0.34	0.94		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
2gii A 224 363 1.2c-63	363	363		1.2e-63				106.53	ZINC FINGER, PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
2gii A 224 391 1.2e-63 C	391 1.2e-63	391 1.2e-63	1.2e-63		0	0.35	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEINDNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEINDNA)
2gii A 260 388 3.4e-34 0.	388 3.4e-34	388 3.4e-34	3.4e-34		o	0.40	0.95		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEINDNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEINDNA)
2gii A 280 418 9e-45 0	418 90-45	418 90-45	9e-45		0	0.13	1.00		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEINDNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEINDNA)
2gii A 288 410 6.8e-31	410 6.8e-31	410 6.8e-31	6.8e-31			0.45	1:00		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
2gli A 99 279 1.5e-42 0	279 1.5e-42	279 1.5e-42	1.5e-42		0	0.14	0.99		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-

PDB annotation	BINDING PROTEIN/DNA)		RIBOSOME 30S RIBOSOMAL SUBUNIT, RIBOSOME, ANTIBIOTIC, CTREED ON PARTY 2	STREFTOM TCIN, 2 SPECTINOMYCIN, PAROMOMYCIN																												
Coumpound			16S RIBOSOMAL RNA; CHAIN: A; FRAGMENT OF MESSENGER BNA, CHARL, Y, 200	RIBOSOMAL PROTEIN \$2:	CHAIN: B; 30S RIBOSOMAL	PROTEIN 53; CHAIN: C; 305	KIBOSOMAL PROTEIN S4;	PROTEIN S5: CHAIN: E: 30S	RIBOSOMAL PROTEIN S6;	CHAIN: F; 30S RIBOSOMAL	PROTEIN S7; CHAIN: G; 30S	RIBOSOMAL PROTEIN S8;	CHAIN: H; 30S RIBOSOMAL	PROTEIN S9; CHAIN: I; 30S	RIBOSOMAL PROTEIN S10;	CHAIN: J; 30S RIBOSOMAL	PROTEIN S11; CHAIN: K; 30S	RIBOSOMAL PROTEIN S12;	CHAIN: L; 30S RIBOSOMAL	PROTEIN S13; CHAIN: M; 30S	RIBOSOMAL PROTEIN S14;	CHAIN: N; 30S RIBOSOMAL	PROTEIN S15; CHAIN: 0; 30S	RIBOSOMAL PROTEIN S16;	CHAIN: P; 30S RIBOSOMAL	PROTEIN S17; CHAIN: Q; 30S	RIBOSOMAL PROTEIN S18;	CHAIN: R; 30S RIBOSOMAL	PROTEIN S19; CHAIN: S; 30S	RIBOSOMAL PROTEIN S20;	CHAIN: T; 30S RIBOSOMAL	PROTEIN THX; CHAIN: V
SEQFOL D score																																
PMF			00:1																													
Verify score			0.78																													
Psi Blast			le-53																													
END			396																													
STAR T AA			217																													
CHAI			ш																													
a a		1	ilig i												_													_				
Se o			1547																							_						
						_	_											_	_		_	_			_	_			_		_	_

PDB annotation			TRANSCRIPTION INHIBITOR BETA- PROPELLER	COMPLEX (ZINC FINGENDNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CYSTAL STRUCTURE, COMPLEX ZINC FINGER (DNA).	COMPLEX (ZINC FINGERIDNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX ZINC FINGERIDNA)	COMPLEX (ZINC FINGERIDNA) ZINC FINGER, PROTEIN-DNA FINGER, PROTEIN-DNA CRYSTAL STUCTURE, COMPLEX CRYSTAL STUCTURE, COMPLEX (ZINC FINGERIDNA)	ZINC FINGER TRANSCRIPTION FACTOR SPI; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI	ZINC FINGER TRANSCRIPTION FACTOR SPI; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFILIA; 5S
Coumpound	RIBOSOMAL PROTEIN RIBOSOMAL PROTEIN SS (PROKARYOTIC) 1PKP 3	RIBOSOMAL PROTEIN RIBOSOMAL PROTEIN S5 (PROKARYOTIC) 1PKP 3	TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	SP1F2; CHAIN: NULL;	SPIF2; CHAIN: NULL;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE;
SEQFOL D score	64.28								
PMF		00'1	0.11	-0.20	60.0	0.18	-0.20	-0.13	0.07
Verify score		0.53	0.31	0.02	-0.41	-0.05	0.21	0.05	-0.63
Psi Blast	Ie-56	Ie-56	0.0045	5.1e-29	5.10-33	1.7e-07	1.7e-10	8.50-09	1.7e-15
END	357	357	219	251	169	104	203	801	130
STAR	211	217	119	172	1.1	77	173	78	69
CHAI N ID			V	U	υ	ອ '			¥
FDB TD	Ipkp	lpkp	lerj	Imey	Imey	Imey	lsp2	1sp2	EJ11
SEQ No.	1547	1547	1549	1553	1553	1553	1553	1553	1553

Coumpound PDB annotation	GENE, NAR, TEILIA, PROTEIN, DNA, TRANSCREPTON FACTOR, SRIA Z GENE, DNA BINDING PROTEIN, ZINC FINGER, COAPLEX 3 (TRANSCREPTON EX) REGULATION/DNA)	C; ADENO-VIRUS PS LEMENT DNA;	N: NULL; ZINC FINGER DNA BINDING DOMAIN DNA BINDING MOTIF, ZINC FINGER DNA BINDING DOMAIN	COOPELEXTRANSCREPTION REGULATION/DIA/) TRAANTRACK FOOTEN (TWO ZNAC-FRICKER PERTIDE) COOPELEXED WITH ZDRP 3	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D; GLI, ZINC FINGER, COMPLEX (DNA; BINDING PROTEINDNA) BINDING PROTEINDNA)	ZINC FINGER PROTEIN GLH; COMPLEX (DNA-BINDING CHAIN: A; DNA; CHAIN: C, D; PROTEINDNA) PIVE-FINGER GLI; GLI, ZHOF FINGER, COMPLEX (DNA-BINDING INCORDANA)
ŏ	CHAIN: E, F;	YY1; CHAIN: ASSOCIATED INITIATOR E CHAIN: A, B;	SWIS; CHAIN: NULL;	COMPLEX(TRANSCRIP REGULATIONDNA) TRAMTRACK PROTEIN ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DI DNA 2DRP 4	ZINC FINGEI CHAIN: A; D	ZINC FINGEI CHAIN: A; D
SEQFOL D score						54.61
PMF		0.24	00:0	0.36	0.03	
Verify		-0.83	-0.36	0.04	-0.30	
Psi Blast		1.46-15	5.1e-06	1.7e-06	3.4e-41	3.4e-41
END		130	104	130	201	229
STAR T AA		49	82	74	25	72
CHAI		υ		A	∢	⋖
PDB CI		1ubd	Izfd	2drp	2gli	2gli
SEQ NO:		1553	1553	1553	1553	1553

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PDB annotation	SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE	CELL DIVISION RCYCLIN H (RECOMBINANT); CYCLIN, CELL CYCLE, CELL DIVISION, NUCLEAR PROTEIN	COMPLEX (ROCIBIN KINASECYCLIN) CYCLIN- BEPRINDENT KINASE-2, COKA, CCNI; COMPLEX (ROCIBIN KINASECYCLIN, CYCLIN, CDK, 2 PHOSPHORYA-ATION, SUBSTRATE COMPLEX		COMPLEX OF TWO ELONGATION PACTORS BE-TU, ET-TS, ELONGATION FACTOR, NUCLEOTIDE EXCHANGE, GTP- BINDING, 2 COMPLEX OF TWO ELONGATION FACTORS	COMPLEX OF TWO ELONGATION FACTORS BE-TJL, BET-TS, ELONGATION FACTOR, NUCLEOTIDE EXCHANGE, GTP- BINDING, 2 COMPLEX OF TWO ELONGATION FACTORS	RNA BINDING PROTEIN G-PROTEIN, BETA-BARREL	RNA BINDING PROTEIN G-PROTEIN, BETA-BARREL	RNA BINDING PROTEIN EFTU;
Coumpound	P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45; CHAIN: B, D;	CYCLIN H; CHAIN: NUIL;	KINASE Z. CHANN. A. C.; C2MITOTIC-SPECIFIC CYCLIN A; CTAIN: B, D; SUBSTRATE; PEPTIDE; CHAIN: E, F;		ELONGATION FACTOR TU; CHAIN: A, B, E, F, ELONGATION FACTOR TS; CHAIN: C, D, G, H;	BLONGATION FACTOR TU; CHANN: A, B, E, E BLONGATION FACTOR TS; CHANN: C, D, G, H;	ELONGATION FACTOR TU (EF- TU); CHAIN: A. B. C. D	ELONGATION FACTOR TU (EF- TU); CHAIN: A, B, C, D	ELONGATION FACTOR;
SEQFOL D score						134.70		131.00	
PMF		0.24	0.28		0.78		1.00		1.00
Verify		-0.49	-0.36		0.02		0.41		0.47
Psi Blast		3e-11	1.5e-09		0	0	0	0	0
END		99	59		541	542	248	552	541
STAR T AA		_	2		122	165	122	124	121
CHAI N ID			g		∢ .	<	٧	٧	٧
PDB ID		ljkw	Iqmz		laip	laip	1d2e	1d2e	1efc
SEQ ID NO:		1558	1558		1559	1559	1559	1559	1559

PDB annotation	TRANSPORT AND PROTECTION PROTEIN, RNA BINDING PROTEIN	RNA BINDING PROTEIN EFTU: TRANSPORT AND PROTECTION PROTEIN, RNA BINDING PROTEIN	COMPLEX (TWO ELDORGATION PACTORS) ELONGATION PACTOR FOR TRANSEER, HEAT UNSTABLE, ELONGATION PACTOR FOR TRANSFER, HEAT STABLE, TELONGATION PACTORS, COMPLEX (TWO ELONGATION PACTORS)	COMPLEX (TWO ELONGATION) RACTORS) ELONGATION FACTOR FOR TRANSFER, HEAT UNSTABLE, ELONGATION FACTOR FOR TRANSFER, HEAT STABLE, ELONGATION FACTOR, COMPLEX (TWO ELONGATION FACTORS)	HYDROLASE ERA, GTPASE, RNA- BINDING, RAS-LIKE, HYDROLASE		TRANSLATION EF-TU; GTPASE, MOLECULAR SWITCH, TRNA, RIBOSOME, Q-BETA REPLICASE, 2 CHAPERONE, DISULFIDE ISOMERASE	TRANSLATION PROTEIN-PROTEIN COMPLEX
Coumpound	CHAIN: A, B;	BLONGATION FACTOR; CHAIN: A, B;	ELONGATION PACTOR TU; CHAIN: A, C; ELONGATION FACTOR TS; CHAIN: B, D;	ELONGATION FACTOR TU; CHAIN: A, C; ELONGATION FACTOR TS; CHAIN: B, D;	GTP-BINDING PROTEIN ERA; CHAIN: A, B;	TRANSPORT AND PROTECTION PROTEIN BLONGATION PACTOR TU (DOMAIN I) - *GUANOSINE DIPHOSPHATE IETU 4 COMPLEX IETU 5	ELONGATION FACTOR TU (EF- TU); CHAIN: A;	ELONGATION FACTOR EEFIA; CHAIN: A; ELONGATION
SEQFOL D score		129.64		115.68		(
PMF			0.86		0.13	0.45	1:00	1.00
Verify			-0.05		0.05	0.18	0.29	0.31
Psi Blast		0	0	0	1.5e-13	8.5e-67	0	0
END AA		542	541	542	368	345	15	542
STAR T AA		137	122	172	126	118	117	120
CHAI N ID		¥	∢	<	¥		<	A
EDB ED		lefc	lefu	lefu	lega	letu	lexm	1f60
SEQ NO:		1559		1559	1559	1559	1559	1559

PDB annotation		TRANSLATION EF-G; BENT CONFORMATION, VISIBLE DOMAIN III, MUTATION HIS573ALA	TRANSLATION TRANSLATIONAL GTPASE		HYDROLASE TETRATRICOPEPTIDE, TTRF, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE.	TRP; HYDROLASE, PHOSPHATASE,	TPR, 2 SUPER-HELIX, X-RAY	STRUCTURE	CHAPERONE HOP, TPR-DOMAIN,	REPEAT, HSP90, 2 PROTEIN	BINDING	CHAPERONE HOP, TPR-DOMAIN,	PEPTIDE-COMPLEX, HELICAL	REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN,	PEPTIDE-COMPLEX, HELICAL	REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN,	PEPTIDE-COMPLEX, HELICAL	REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN,
Coumpound	FACTOR EBF1BA; CHAIN: B;	ELONGATION FACTOR G; CHAIN: A;	TRANSLATION INITIATION FACTOR IF2/EIF5B; CHAIN: A;		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN	PHOSPHATASE 5; CHAIN:	NOLL;		TPR2A-DOMAIN OF HOP;	MEEVD; CHAIN: B:		TPR2A-DOMAIN OF HOP;	CHAIN: A; HSP90-PEPTIDE	MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP;	CHAIN: A; HSP90-PEPTIDE	MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP;	CHAIN: A; HSP90-PEPTIDE	MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP;
SEQFOL D score																						
PMF		0.00	0.28		0.07	0.83				0.70			0.03			0.10			0.41			0.05
Verify score		-0.15	0.03		0.08	-0.01				10.01			-0.46			-0.07			95.0			-0.02
Psi Blast		1.7e-05	8.5e-62		4.5e-09	1.2e-06				1.3e-08			0.0012			0.003			0.0003			0.0001
END	_	459	553		591	105				Ε			401			558			611			165
STAR T AA		319	123		61	2				61			316			462			54			63
CHAI N ID		<	٧							4			٧			Ý			V			٧
PDB ID		1fnm	1g7s	İ	1817	la17				leir		ĺ	lelr			Ielr			lelr			leir
SEQ ID NO:		1559	1559		1561	1991			1	1961			1991			1991			1561			1991

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PDB annotation	PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	SIGNALING PROTEIN PEROXISANORE RECEPTOR 1, PTS1- BR, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRARITACOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR,
Coumpound	CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR1-DOMAIN OF HOP; CHAIN; A, B; HSC70-PEPTIDE; CHAIN; C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: A, B; PTSI-CONTAINING PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: A, B; PTSI-CONTAINING PEPTIDE; CHAIN: C, D;
SEQFOL D score								
PMF		86.0	0.71	0.95	0.19	0.12	0.65	0.31
Verify score		0.38	0.26	0.31	-0.68	0.41	0.25	0.34
Psi Blast		7.5e-08	5.1e-06	4.5e-07	0.00034	1.7e-05	1.36-13	1.2e-10
END		119	123	97	472	537	252	611
STAR		19	25	2	382	458	17	7
CHAI N ID		¥	∢	Ą	٧	¥	∢	¥.
PDB ID		lclw	lelw	lelw	lelw	Ielw	1fch	Itch
SEQ NO:		1561	1951	1561	1561	1561	1561	1561

	TSI.	, TPR,	TSI.	, TPR,	IRT,	C1 F		4		LS,		-	- ;	LS,			D 35
PDB annotation	2 HELICAL REPEAT SIGNALING PROTEIN PEROXISMORE RECEPTOR I, PTSI- BP, PEROXIN-5, PTSI PROTEIN- PEPTITIS COADI IS'	TETRATRICOPERTIDE REPEAT, TPR, 2 HELICAL REPEAT	SIGNALLING PROTEIN PEROXISMORE RECEPTOR I, PTSI- BP, PEROXIN-5, PTSI PROTEIN-	PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT,	CHOLESTEROL METABOLISM, 2	ACTIVATION	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS, STRIICTHRAL, PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 2.2	I ANDEM 3-HELLA COLLED-COLLS, STRUCTURAL PROTEIN	ENDOCYTOSIS/EXOCYTOSIS	NSECI; PROTEIN-PROTEIN COMPLEX MILITI-SUBLINIT	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35
Coumpound	PEROXISOMAL TARGETING SIGNAL I RECEPTOR, CHAIN: A, B; PTSI-CONTAINING BEPTINE: CHAIN: C, D.	DEPOXICOALLI TAROPENIO	PEROMINAL TARGETING SIGNAL I RECEPTOR; CHAIN: A, B; PTSI-CONTAINING	PEPIIDE; CHAIN: C, D;	A, B, C, D;			ALPHA SPECTRIN; CHAIN: A,	វ័		ALPHA SPECTRIN; CHAIN: A,	В, С;			SYNTAXIN BINDING PROTEIN	I; CHAIN: A; SYNTAXIN IA; CHAIN: B:	SYNTAXIN-1A; CHAIN: A, B, C;
SEQFOL D score					16:89			68.37									
PMF	0.03	9	0.48								0.03				0.10		0.00
Verify score	0.05	9	0.10								0.04				-0.33		0.19
Psi Blast	3.4e-10	1.45	1.46-11		1.4c-07			1.5e-10			1.5e-10				1.5e-13		1.5e-07
END AA	563	700	780		242			233			569				254		128
STAR T AA	318		i .		- 4			61			19				18		s
CHAI N ID	A		€		∢			٧			V				д		∢
PDB ID	1fch	100	nor i		lavl			lcnn			lcm				ldn1		lez3
SEQ ID NO:	1561	1551			1563			1563			1563				1563		1563

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PDB annotation	KDA PROTEIN, P35A, THREE HELLY BUNDLE	PROTEIN TRANSPORT HELIX- TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT	CONTRACTILE PROTEIN TRIPLE- HELIX COLLED COIL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COLLED COIL, CONTRACTILE PROTEIN	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION		COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-MING), HYDROLASE 2, MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITORNUCLEASE) COMPLEX (INHIBITORNUCLEASE), COMPLEX (R.HARDANG), HYDROLASE 2 MOLECULAR RECOGNITION, BRITOPE MAPPING, LEUCNE-RICH 3 REPEATS	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP.RBD OR RRM) AND LEUCINE-RICH- REPEAT2 (LRR)	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45: CYCLIN
Coumpound		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;		KIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L,
SEQFOL D score		80.09	71.18							
PMF				90:0-	0.12		0.00	0.62	-0.05	0.01
Verify score				0.01	60.0		90.00	0.50	0.04	90'0
Psi Blast		1.2e-09	4.5e-17	4.5e-17	1.2e-06		1e-13	1.5e-13	6.8e-09	3.46-15
END AA		283	291	246	287		143	176	133	140
STAR T AA		2	22	5	92		11	8	43	3
CHAI N ID		4	∢	<			¥	⋖	В	٧
PDB ID		1qqe	lquu	lquu	Isig	_	la4y	la4y	1fo1	1fqv
SEQ NO:		1563	1563	1563	1563		1565	1565	1565	1565

	ó,	26.	4				
PDB annotation	A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN ACDK2. ASSOCIATED PROTEIN P45, CYCLIN ACDK2-ASSOCIATED PROTEIN P19, SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REBEATI, SCF. UBROUTTIN; 2 E3, UBIOUTTIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2. ASSOCIATED P49, CYCLIN A/CDK2. ASSOCIATED P49, SYP1, SXP2, F. BOX, LRRS, LEUCINE-RICH REPEATS, SCR, 2 UBGOUTH). E3, UBIOUTHY PROTEIN LIGASE	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS		
Coumpound	N, P;	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, I, L, N, P;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	RIBONUCLEASE INFIBITOR; CHAIN: NULL;	LYASE(OXO-ACID) CARBONIC ANHYDRASE II (E.C.4.2.1.1) (50 MM TRIS, 2CBA 3 3 M AMMONIUM SULFATE, PH 7.8) 2CBA 4	LYASE(OXO-ACID) CARBONIC ANHYDRASE II (B.C.4.2.1.1) (50 MM TRIS, 2CBA 3.3 M AMMONITM SUILFATE, PH 7.8)
SEQFOL D score				,			403.66
PMF		0.99	0.07	0.03	0.35	1.00	
Verify score		0.74	0.23	0.01	0.18	1.12	
Psi Blast		3e-17	3.46-15	1.5e-12	4.5e-10	0	0
END		174	140	143	176	242	242
STAR T AA		e.	es .	11	2	en	e.
CHAI N ID		∢	∢				
PDB ID		Ifqv	162	2bnh	2bnh	2cba	2cha
SEQ ID NO:		1565	1565	1565	1565	1567	1567